

Sequence Listing

111> Baker, Kevin P.  
 Benstein, David  
 Desnoyers, Luc  
 Eaton, Dan L.  
 Ferrara, Napoleone  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Gagnard, Audrey  
 Godowski, Paul J.  
 Grimaldi, Christopher J.  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Pan, James  
 Paoni, Nicholas F.



0120> Secreted and Transmembrane Polypeptides and Nucleic  
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                  170                 175                 180  
  
 Gly Leu Ala Leu Glu Ile Arg Ser Leu  
                  185

<210> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

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ttctgtggac tegttaaagga aaactaaaga ttgaagacat cactgataag 200  
tacattttta tcactggatg tgactggggc ttgggaaact tggcagccag 250  
aaattttgat aaaaagggat ttcatgtaat cgtgcctgt ctgactgaat 300  
caggatcaac agctttaag gcagaaacct cagagagact tegtactgtg 350  
cttctggatg tgaccagccc agagaatgtc aagaggactg cccagtgggt 400  
gaagaaccaa gttggggaga aaggctctctg gggctctgac aataatgctg 450  
gtgttccgg cgtgctggct cccactgaat ggctgacact agaggactac 500  
agagaacctt ttgaagtga cctgtttgga ctcatcagtg tgacactaaa 550  
tatgcttctt ttggtcaaga aagctcaagg gagagtatt aatgtctcca 600  
gtgttgagg tgcctttgca atcgttgag ggggtatac tccatccaaa 650  
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tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaaattgg 750  
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tctccagaca tcaaacacaa atatggagaa ggttacattg aaaaaagtct 850  
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gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050  
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gtatttaggc tttgctgct tgggtgatg taagggaat tgaaagaatt 1350  
gccattcaa aatgatcttt accgtggcct gcccatgct tatggtccc 1400  
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aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
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<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 36-47, 108-113, 166-171, 198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature  
<222> 39-42  
<223> Glycosaminoglycan Attachment Site.

<230>  
<231> TRANSMEM  
<232> 136-152  
<233> Transmembrane Domain

<230>  
<231> misc\_feature  
<232> 161-163, 187-190 and 253-256  
<233> N-glycosylation Sites.

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Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala  
35 40 45  
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys  
50 55 60  
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu  
65 70 75  
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val  
80 85 90  
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly  
95 100 105  
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala  
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val			

02100 11  
 02110 2720  
 02120 DNA  
 02130 Homo sapiens

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 ggccttggg ccgtcgccac cactgtagtc atgtaaccac cgcgcgcgc 150  
 ggggctcat cgggaacttc tctcgggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggggggggt cgtgctggag gaaatggaag 250  
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gtttttctgt ggactctctt ttacatcaa ctgggtgac cattggaaag 350  
ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
gggttaaaaac cagcaaatcc accgtctta ccagctctc agaaggcgga 450  
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catggaaagg ataccgcaag tttgcctggg gccatgacga gctgaagcct 850  
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ccacctgtct ggggacagcc tcttctgag gaaagctgag gattttggaa 1100  
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 aacctgctca gcttggagc ctactgttc aacacagaag cccacctct 2100  
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 cctctgggc gccccgagg gggcttggag ggtggagcg caagtcctc 2650  
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

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	20	25	
Val Ala Thr Thr	Val Val Met Tyr Pro Pro Pro Pro Pro Pro		45
	35	40	
His Arg Asp Phe	Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr		60
	40	55	
Asp Asn Ser Lys	Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp		75
	65	70	
Lys Gln Leu Ser Arg	Leu Gln Arg Asn Met Ile Leu Phe Leu Leu		90
	80	85	
Ala Phe Leu Leu Phe	Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala		105
	95	100	
Asp His Trp Lys	Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys		120
	110	115	
Met Arg Pro Glu	Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val		135
	125	130	
Leu Pro Ala Pro	Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro		150
	140	145	
Glu Ile Ser Ser	Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro		165
	155	160	
Pro His Leu Gln	Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly		180
	170	175	
Thr Gln Glu Glu	Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro		195
	185	190	
Arg Pro Glu Gly	Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly		210
	200	205	
Ala Val Ile Glu	Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg		225
	215	220	
Ala Glu Val Pro	Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln		240
	230	235	
Gly Thr Pro Val	His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp		255
	245	250	
Val Phe Leu His	Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly		270
	260	265	
His Asp Glu Leu	Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe		285
	275	280	
Gly Leu Gly Leu	Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile		

	290		295		300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser		
	305		310		315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu		
	320		325		330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu		
	335		340		345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn		
	350		355		360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser		
	365		370		375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr		
	380		385		390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe		
	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala		
	410		415		420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425		430		435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
	440		445		450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455		460		465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470		475		480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485		490		495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val		
	500		505		510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515		520		525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
	530		535		540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545		550		555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560		565		570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		

575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690
His Pro Leu Pro Ile Trp Thr Pro Ala		
695		

<110> 13

<111> 24

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gogtgattga cgtc 24

<110> 14

<111> 24

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gcgc 24

<110> 15

<111> 44

<112> DNA

<113> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggctct tcagttagtg gtttggctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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gcgcagctgc cctgggagga cggcaggtec gggttgctct cggcgggcct 150  
cctcggaag tgttcctct tccacctgtt cgtggcctgc ctctcgctgg 200  
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cccacgcct ggcagtgctg gtgcctctcc gogaacgctt cgaggagctc 400  
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gcaccacat taagtctca accaggtgga caacttcagg ttcaaccggg 500  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
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 <212> PFT  
 <213> Hemo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

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 20 25 30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
 35 40 45

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala		
				50					55					60		
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys		
				65					70					75		
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp		
				80					85					90		
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe		
				95					100					105		
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser		
				110					115					120		
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp		
				125					130					135		
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu		
				140					145					150		
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp		
				155					160					165		
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala		
				170					175					180		
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His		
				185					190					195		
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His		
				200					205					210		
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly		
				215					220					225		
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu		
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Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe		
				245					250					255		
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg		
				260					265					270		
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly		
				275					280					285		
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu		
				290					295					300		
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp		
				305					310					315		
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser					
				320					325							

<210> 18  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
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<210> 19  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
ggagtgcggg aagcacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
cttcttgagg aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gactggtcgg tgcccagaaa gtctctttctg ccactgaagg ccccatcagg 150  
gatgggacct tctttccccc ttctttttctg tgtctctgc ctcatgggc 200  
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attatataaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> ERT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc\_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly  
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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30

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35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
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Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
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<210> 23

<211> 2383

<212> DNA

<213> Homo sapiens

<400> 23

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ggtcggggg aggcgcgta ggcagtgag ccgcgcctcg ccgcgcggc 200

ccgcgcgcgc agcatggag caccgggag ccggcggggc cgcgcgcgc 250

cgcgcgtgtt gctgcgcgc togtgttag cgtgtgtgc gctgtgtgga 300

ggcgggggg gggcggggc cgcgcgcgtg ccgcgcgggt gaaagcgc 350

tggcgggccc cgaggggctg gcagggcggc gggcgccgac gagggcagg 400

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 <211> 616  
 <212> PRT  
 <213> Homo sapiens

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 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<4000> 24

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Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His	35	40	45	
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	50	55	60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	65	70	75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	80	85	90	
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	140	145	150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	155	160	165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	170	175	180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	185	190	195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	200	205	210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	215	220	225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	230	235	240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	245	250	255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	275	280	285	

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Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln
				305					310					315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg
				320					325					330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser
				335					340					345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp
				350					355					360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln
				365					370					375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro
				380					385					390
Gln	Asp	Glu	Arg	Lys	Ala	Trp	Arg	Arg	Cys	Asp	Arg	Gly	Gly	Phe
				395					400					405
Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val
				410					415					420
Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr
				425					430					435
Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu
				440					445					450
Ala	Ala	Asn	Phe	Ser	Asp	Lys	Met	Asp	Val	Ile	Phe	Val	Ala	Glu
				455					460					465
Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys
				470					475					480
Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu
				485					490					495
Ala	Asp	Glu	Arg	Val	Leu	Trp	Leu	Ala	Gln	Arg	Glu	Ala	Lys	Ala
				500					505					510
Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg
				515					520					525
Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile
				530					535					540
Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met
				545					550					555
Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly
				560					565					570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys  
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu  
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr  
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Ser

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<220>  
<223> Synthetic oligonucleotide probe

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<220>  
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<400> 26  
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<212> DNA  
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<210> 28  
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<212> DNA  
<213> Homo sapiens

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gcagaggctt cgtgagggag ttatcagaga cattgagagg caaattcgga 150

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 <211> 81  
 <212> FRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

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 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
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 Lys Gly Ser Gln Lys Ser  
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 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30

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<211> 322  
<212> PRT  
<213> Homo sapiens

<400> 31  
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35 40 45  
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
50 55 60  
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
65 70 75  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
80 85 90  
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	
	110	115 120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp		
	125	130 135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala		
	140	145 150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile		
	155	160 165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu		
	170	175 180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn		
	185	190 195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr		
	200	205 210
Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu		
	215	220 225
Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu		
	230	235 240
Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu		
	245	250 255
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln		
	260	265 270
Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr		
	275	280 285
Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr		
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His Leu Val Phe Val Lys Val		
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<210> 32

<211> 3580

<212> DNA

<213> Homo sapiens

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<E10> 33

<E11> 335

<E12> PRT

<E13> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

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<210> 35  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 35  
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<210> 36  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 36  
ttccactcaa tgagggtgag cactc 25

<210> 37  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 37  
ggcagagccct aactatccag gag 23

<210> 38  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 38  
ggagatcgct gcgctggcca ggtcccccct gcatggat 39

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
ctggtgcaaa gcgagctct tg 22

<210> 40  
<211> 2084

<212> DNA

<213> Homo sapiens

<410> 41

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ccatctgttt totctaagc agcacagatt cctttcagac aggacaaatg 150  
tgatatttca ctctctgatt gtaaatcct ccttaagcctg aagcttctgt 200  
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caaagtgttt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tcttttgaaa gtgaagcaaa cttaaaactc gataaagaaa 500  
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ccttgatcca tagctttgtt totaaagtgc ctgtggaatgc acctatagca 700  
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<210> 41  
 <211> 334  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
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 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
 35 40 45  
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
 50 55 60  
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
 65 70 75  
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
 80 85 90  
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
 95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val	110	115	120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser	125	130	135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr	140	145	150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser	155	160	165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val	170	175	180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser	185	190	195
Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu	200	205	210
Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn	215	220	225
Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe	230	235	240
Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu	245	250	255
Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser	260	265	270
His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu	275	280	285
Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser	290	295	300
Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu	305	310	315
Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu	320	325	330

Arg Thr Ser Val

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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ccctataata aattttactc tatacaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

	230		235		240									
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile
			245						250				255	
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu							
			260											

<210> 44  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 44  
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<210> 45  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
 gggaaatgct atctgatgcc 20

<210> 46  
 <211> 16  
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 <223> Synthetic oligonucleotide probe

<400> 46  
 caggatctcc tcttgacgtc tgcagc 26

<210> 47  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 47  
 cttctcgaac cacataagtt tgaggcag 28

<210> 48  
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<220>

<223> Synthetic oligonucleotide probe

<400> 48

caactattccc tccacagcaaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

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cgggagcacc cagtctgta cgccaaggaa ctggctctgg gggcaccatg 150  
gtttcggcgg cagccccag cctctcctc cttctgttgc tgetgetggg 200  
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 aaaaaaaaaa aaaaaaaga 1969

\*210\* 50

\*211\* 283

\*212\* PRT

\*213\* Homo sapiens

\*400\* 50

Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
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Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu  
 20 25 30

Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45

Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60

Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75

Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

80										85					90				
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala					
				95					100					105					
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln					
				110					115					120					
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys					
				125					130					135					
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe					
				140					145					150					
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala					
				155					160					165					
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr					
				170					175					180					
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp					
				185					190					195					
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys					
				200					205					210					
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro					
				215					220					225					
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu					
				230					235					240					
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly					
				245					250					255					
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro					
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<212> DNA

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Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
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Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
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Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
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Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
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Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
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Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
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Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
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Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
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Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
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Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195

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				200					205					210

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				215					220					225

Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240

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Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	340	345
Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
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<211> 3580

<212> DNA

<213> Homo sapiens

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\*400\* 54  
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Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu	155	160	165
Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu	170	175	180
Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala	185	190	195
Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg	200	205	210
Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala	215	220	225
Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp	230	235	240
Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala	245	250	255
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<212> DNA

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\*210\* 58

\*211\* 1115

\*212\* PRT

\*213\* Homo sapiens

\*400\* 58

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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
			20					25					30	

Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
			35					40					45	

Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
			50					55					60	

Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
			65					70					75	

Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
			80					85					90	

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln	95	100	105
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala	110	115	120
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln	125	130	135
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys	140	145	150
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val	155	160	165
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met	170	175	180
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu	185	190	195
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val	200	205	210
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr	215	220	225
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile	230	235	240
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser	245	250	255
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser	260	265	270
Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly	
				665					671					675	
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu	
				680					685					690	
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr	
				695					700					705	
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr	
				710					715					720	
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met	
				725					730					735	
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr	
				740					745					750	
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys	
				755					760					765	
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His	
				770					775					780	
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn	
				785					790					795	
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr	
				800					805					810	
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro	
				815					820					825	
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg	
				830					835					840	
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro	
				845					850					855	
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	

Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	1100	1105	1110
Pro	Pro	Leu	Thr	Ile											1115		

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<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgtgtg gaggc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 61  
aacacaaaag cccaggctccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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cacgggcccc gaggggtccc ggcgcctcag ccggcggtat ctggggcgtc 150  
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<210> 63

<211> 437

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg
				20				25					30	

Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35				40					45	

Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50				55					60	

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro			
				65					70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser			
				80					85					90			
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg			
				95					100					105			
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe			
				110					115					120			
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val			
				125					130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp			
				140					145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His			
				155					160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala			
				170					175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val			
				185					190					195			
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser			
				200					205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys			
				215					220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met			
				230					235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val			
				245					250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala			
				260					265					270			
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Gln	Val	Ser	Gln	Ala	Pro			
				275					280					285			
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu			
				290					295					300			
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly			
				305					310					315			
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu			
				320					325					330			
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg			
				335					340					345			

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp	350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu	380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val	410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser	425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val	440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala	455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro	470	475	480
Thr Phe Thr Gln Trp Leu Cys	485		

<210> 64  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <210> 65  
 <211> 25  
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 gtcacacaca gctctggcag ctgag 25  
  
 <210> 66  
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 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 4"

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa ggcctgataag catgaagctc ttatctttgg tggctgtggt 150  
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tcgggtgcaa atgcctctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
gcccattgca gtgcctggcc atgacgtgga ggctactgc ctgctgtgog 350  
agtgcaggta caggagagcg agcaccacca ccaccaaggt caccattgtc 400  
atctacctgt ccgtgggtggg tgcctgttg ctctacatgg ccttctgtat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
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ccagcagcgg tggaaagtgc aggtgcagga gcagcggag acagtcttcc 650  
atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggcctgcagc ttccaggctg gacaaagcag ggggtactt 750  
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ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
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 cgtgttcccc tgtgcaacttc tgcactggg gcctggagtg cccatgcata 1300  
 ctctgtctgc ggtccccctca cctgcaacttg aggggtcttg gcagtccttc 1350  
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 gactcgagga tgagcgtgga tctgaacacc acagccctg taattgggtt 1450  
 gctctttgtc cctgaacttc gttgtaccag tgcctggaga gaaaattttg 1500  
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<210> 63  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
 20 25 30  
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
 35 40 45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
 50 55 60  
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
 65 70 75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
 80 85 90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
 95 100 105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
 110 115 120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
 125 130 135  
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
 140 145 150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
 155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
 170 175 180

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 tctgcaagcc ccgcgaccc aagtgagggg ccccggtgtt gggtcttccc 150  
 tccctttgca tcccacccc tccgggtttt ggttcttctt ggggaccccc 200  
 tcgcggggag atggccgcgt tcatgaggag caaggattcg tctgctgccc 250  
 tgcctctact ggcgcgggtg ctgatgggtg agagctcaca gatcggaagt 300  
 tcgggggcca aactcaactc catcaagtcc tctctggggg gggagaagcc 350  
 tggtcaggcc gccaatcgat ctgoggggcat gtaaccaagga ctggcattcg 400  
 ggggcagtaa gaaggggcaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttag gaggtattgc cacagtcccc accaaggatc 500  
 atcgggctgc atggtgtgtc ggagaaaaaa gaagcgtctc caccgagatg 550  
 gcatgtgtg cccagtaac cgtgcaata atggcatctg tatccagtt 600  
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 tcattttctg accaaaatct gcaaacccag gtccatcag ggggaagtct 850  
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 tggaactgtg cgaagggcct gtcttgcaaa gtatggaaa atgccaacta 950  
 ctctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
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 catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100

gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caaattgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
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gctaacagag agatcattat ttcttaaaga ttggccataa cctatatatt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgttggaat 2000  
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aggcacaagt tggctgttca ttttgaaac caggggatgc acagtctaaa 2150  
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tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
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 ttttttactt aaatcccatc tgcagttcca aatttaagtt ctcccagtag 2700  
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 atataacaat tatttatattt acaatttggt ttctgcaata tttttcttat 2950  
 gtccacccctt ttaaaaatta ttatttgaag taatttatatt acaggaaatg 3000  
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
 gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
 taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150  
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
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 Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
 20 25 30  
 Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
 35 40 45  
 Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
				245					250					255

Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 apatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 ctcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200  
 tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250  
 atattitagt aattcatatg ttttagatta taggttttaa catacttggtg 300  
 aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
 ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400  
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
 tttggaccag ttgaaagctc cgagtgttgg ccagtttacc accaccccaa 500  
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550

ctcaaggccc caacatccca gtcttcagtc ctccagtcato ttgaattcaa 600  
 atctcaacct gagcatccc cagttcttag ccagtttgagc cagcgacaac 650  
 agcaccagag ccaggccagtc actgttccctc ctcttggttt ggagtccttt 700  
 ccttcaccagg caaaaacttcg agaatcaaca ctctggagaca gtccctccac 750  
 tgtgaacaag cttttgcagc ttcaccagac gaccattgaa aatatctctg 800  
 tgtctgtcca ccagccacag cccaaacaca tcaaaccttg taagcggcgg 850  
 atacccccag cttctaagat ccagcttct gcagtggaac tgcttggttc 900  
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttggtt 950  
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaatatagt 1000  
 aatcagattc ccacagctt gtattcgaag tctttaagtg agcctttgaa 1050  
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 ccgtcattac ctctgcagt ctgacaagct catcactgaa ttctgctagt 1150  
 ccagtagcaa tgtcttccctc ttatgaccag agttctgtgc ataacaggat 1200  
 ccataccaa agcctgttga gttcatcaga gtcagctcca ggaaccatca 1250  
 tgaatggaca tgggtggtgtt cgaagtcagc agacactaga cagtaagtat 1300  
 agcagcaagc tactcttgtc atggctggtg ccaaccaaaac agaggaagag 1350  
 gatagctcac gtgatgttga aaacaccagt tggccaatgg ctcatctgtt 1400  
 aaaagcagc ccttttgctt ttttgttttt ggaccaggtg ttggctgttg 1450  
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 ttctctctgc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550  
 tttaaagatg cttggggccag ggggggttgg tgatgccat aatcccagtg 1600  
 ctttgggggg ccaaggcagg cagattgcc aagctcagga gtttgagacc 1650  
 accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
 gcggggtgtg gtggcgggcg gtgcctgtaa tccagctac ttgggaggct 1750  
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
 ctgaaaaga 1809

<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

	275		280		285
Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr Gln			
	290		295		300
Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met Asn			
	305		310		315
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys Tyr			
	320		325		330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln Arg			
	335		340		345
Lys Arg Ile Ala	His Val Met Trp Lys	Thr Pro Val Gly Gln Trp			
	350		355		360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 73  
 aaattcatggc aaatatttcc ctcccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
 tggataaactg gcccaaaactc gg 22

<210> 75  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
 nttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens

411> 76

gcccagctggg acaaaagcccg gggctggggg gggggccatgg cgtgcacac 50  
ccgaatcccg ctttggaacac ttgtgattct ggaagatctt gctgttctcc 100  
tgcaactcagc ggtggaggag acggacgggg ggtgtacac ctgcaacctg 150  
caccatcact actgcacact ctacgagagc ctggccgtcc gctggagggt 200  
caccgaaggc ccccgggcca ccccgcccta ctgggaaggc gagaaggagg 250  
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 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77  
 <211> 341  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
 Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
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 Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
 20 25 30  
 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
 35 40 45  
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
 50 55 60  
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
 65 70 75  
 Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
 80 85 90  
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
 95 100 105  
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
 110 115 120  
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
 125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78  
 <211> 2143  
 <212> DNA  
 <213> Homo sapiens

<400> 78  
 agcgggaggc agcgggggag tggcgacagc ggcacatggc cgttgtctca 5'  
 gaggacgact ttcagcacag ttcaaaactcc acctacggaa ccacaagcag 100  
 cagtctccga gotgaccagg aggcactgct tgagaagctg ctggaccgac 150  
 agccccctgg cctgcagagg ccgaggagcc gcttctgtgg cacatacatc 200

atctctcttca gcttggggcat tggcagtcta ctgcatgga acttctttat 250  
 cactgccaag gactactgga tgttcaaat ccgcaactcc tccagcccag 300  
 ccaacgggga ggacccagag ggcacagaca tcttgaacta ctttgagaga 350  
 taccttgccg ttgcctccac cgtgcctccc atgtgtgtgc tggtaggcaa 400  
 ctctctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
 tgaaggctat cctggccatc ttcatgtga taactgcat ggtgaaggtg 500  
 gacacttctt cctggacccg tgggtttttt ggggtcacca ttgtctgcat 550  
 ggtgatctc agcgggtgct ccactgtctt cagcagcagc atctacggca 600  
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 gccatggggc ggaaggtag cggcgtggcc tcattgggtg acttggctgc 700  
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 gattcattga ttccacaca cccctctccc gcccatctt gaagaagacg 950  
 gccagcctgg gcttctgtgt cactacgtc ttcttcatca ccagcctcat 1000  
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 taaagtttca cttggggaca gagagcagag cacactcggg cctcatcct 1600  
 cccaagatgc cagtgaacca cgtccatgct cattccgtgc aaggcagata 1650

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 ggcagtgcca aaacccagcc atgggctctt tgcacccctc cagctgogct 1850  
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 gaaggggtct ccttggaatg gaagtcacct ggcctgggta gtctcagga 1950  
 ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000  
 ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050  
 cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
 agcctggggt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150  
 cctgggtcaa gatgagggtc ttccagtgtt cctgtttaca acatgtcaaa 2200  
 cccattgggt caaggcgcta ataaatactt gcgtattcaa aaa 2243

<110> 79  
 <111> 475  
 <112> PET  
 <113> Homo sapiens

<100> 79  
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 20 25 30  
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 35 40 45  
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
 50 55 60  
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
 65 70 75  
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
 80 85 90  
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
 95 100 105  
 Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val  
 110 115 120  
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val  
 125 130 135

Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys	395	400	405
Thr	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

<210> 80  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 80  
 ttttgggggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 81  
 ggttaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 82  
 taaggcatga cgggtctctt tcttatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 ctggagacac catctccac ccagagtcct ggcccattg gccctgcacc 100  
 tctctgtct ctctccctc ctctcagcc tggtaggctc ccaggactgg 150

aagggtgaac gtagccaaga ccccttcag agatgcatgc aggatcctga 200  
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agccccagag ggtgattgtg gttggcctg gtgtggcctg gctggtggcc 300  
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cgacaajaac acgtggacgg aggtgcacga agtgaagctg cgcactatg 550  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

(210) 84  
 (211) 567  
 (212) PRT  
 (213) Homo sapiens

(400) 84  
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 1 5 10 15  
 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln  
 20 25 30  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165  
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr	200	205	210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala	215	220	225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr	230	235	240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp	245	250	255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro	260	265	270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala	275	280	285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln	290	295	300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala	305	310	315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile	320	325	330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg	335	340	345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg	350	355	360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn	365	370	375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu	380	385	390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala	395	400	405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu	410	415	420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp	425	430	435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser	440	445	450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu	455	460	465
Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly	470	475	480

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
				560					565					

<210> 35  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
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 gaactcagag ccgggaagcc ccattcact agaagcactg agagatgcgg 200  
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 tgtctgacaa tgggcctctg ttgggatata gaaaaccaa ccagccctac 550  
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
 ctgtctcttg cataaagggt ataatcctc accagaccag ttgtcggca 650  
 tctttgtcca gaataggcca gactggatca tctccgaatt ggcttgttac 700  
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750  
 catcgtacat attgtcaaca aggtgatat cggcatgggt atctgtgaca 800  
 ccccccaaaa ggcattgggt ctgataggga atgtagagaa aggtttcacc 850

cagagcttga aggtgatcat ccttatggac ccccttgatg atgaactgaa 900  
gcaaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgtg 950  
agaactagg caaagagcac ttcagaaaaa ctgtgcctcc tagccagaa 1000  
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cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250  
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 aaaaactatt cttacatttg ttttgccctt cctcctatct ttttttaacc 2400  
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 tctaatatt aaggcttcag ggtactttt atcaacatgc ctgtcttcaa 2550  
 gatcccagtt tatgtttctgt gtccttcctc atgatttcca accttaatac 2600  
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 aaatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150  
 acaggcaagc aagatgtcca cacaacaggc ttattttctg tgaaggaaac 3200  
 aactgatctc ccccacctt ggattagagt tctgtctca ccttaccac 3250  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25				30	

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile					
50										55					60				
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys					
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Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly		
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<213> Homo sapiens

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 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
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 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
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Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His	245	250	255
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Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro	350	355	360
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 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
 185 190 195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
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Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	
				230					235					240	
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	
				245					250					255	
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	
				260					265					270	
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	
				275					280					285	
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	
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<211> 401

<212> PRT

<213> Homo sapiens

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
				80					85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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230	235	240
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245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
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Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
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Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
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 <212> DNA  
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<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
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Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
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Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
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Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
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Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
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Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
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Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
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His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
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Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
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Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
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Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
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Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
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Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
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Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	
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Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	
				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
				485					490					495	
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
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Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
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Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
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Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
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Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
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His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
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Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
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Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
				665					670					675	
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
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Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
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Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	

Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Gln	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg  
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Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe  
1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly  
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<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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cttatccatc aacatgaaga atgtccatac atggactcca ccagaggggc 150  
ttcaaggagt taaagttact tacaactgtc agtatttcac caccattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt ttgtttgtcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tctgtttcc 300  
atgcaacaaa tatactocaa ttggaagtat aactgtctct tttgaatac 350  
taaatacaac agaactgggt cccagtgtgt gaccaaccac acgtgtgtgc 400  
tcaactgggt ggagccgaac actctttact ggtacacgt ggagtccctc 450  
gtcccagggc cccctgcgcg tgctcagcct ttgagaagc agtgtgccag 500  
gaatttgaaa gatcaatcat cagagtcca ggtaaaaac atctttctgt 550  
atgttttgcg catatctatt accgtgttcc tttttctgt gatgggtat 600  
tccatctacc gatatacca cgttggcaca gagaaacac cagcaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcaccctca atatctgga tgattctaaa 750  
atttctcacc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
cttaatgat cctcagccca gggggaacct gagggccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttgc atttgatgga aattttttgt 900

gactctgaag aaaaacaggga aggtacttct ctaccccagc aagagtcctt 950  
 cagcagaaca ataccccagg ataaaaacagt cattgaatat gaatatgatg 1000  
 tcagaaccac tgacatttgt ggggggcttg aagagcagga gtcagtttg 1050  
 caggaggagg tgtccacaca aggaacatta ttggagtgcg aggcagcgtt 1100  
 ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150  
 aagaactaga cccctggcg caggagcaca caactcggga ggaggggcgg 1200  
 gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250  
 gctgtgtatt ccttcgtgtt ccagcttcga ccaggattca gagggctgcg 1300  
 agccttctga gggggatggg ctoggagagg agggcttctt atctagactc 1350  
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggcat ggggggtata tgtgcagatg gaaaactgat 1450  
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 cctttgatcc cagccataaa gtacctggga tgaaagaagt ttttccagt 1550  
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 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atggtgggcc 1650  
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 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104  
 <211> 442  
 <212> PRT  
 <213> Homo sapiens

<400> 104  
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 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu  
 20 25 30  
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr  
 35 40 45  
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser  
 50 55 60  
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu  
 65 70 75  
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His  
 80 85 90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
381 385 390

Gly Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgctgctgct gttgctcttg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

caatgtgcca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtaggagga agcggttg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108  
ctctccgag tctgtgtgt cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 109  
ggaggggag ttccctgtgt ctctgggtgt ttgcctaaac ctgcaaacat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
ggaggggtg gggggaggg tgggggagc cgtgggtctc tgcggggaga 50  
ggccagcctg cgtctgcctt ggggtctggg ttgaggggtt ggggacgtcc 100  
tctgttgact gtggccaccc cctgatgtgt gccctgaag ccccccagc 150  
gtctctgggg ggcacagatc atggggggcc acgaggtgac ccccaactcc 200  
aggccctaca ttgcctcctt gctcttctgg ggcacacatc actggggagg 250  
cttctgtgtg cagagccctt ggttgggtct ggcggccccc tcttccagcc 300  
acagagacct ccgcaactgg ctggtgggtg tggggggccc cgtcttgagt 350  
actggggagc ccccccagca ggtgttttgg atcgatgtct tcaccacgca 400  
ccccgaactc ccccccatga cccacgccc cagacatctg ctgctggggc 450  
tgaaaggctc tctgttcttg ggcctcagc tggggctgtt gaggctgcca 500  
gggagaaggg ccaggccccc caccggggg acacgggtgc ggggtggctgg 550  
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600  
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gggtcttctg cgggcagact ccggagggcc cctggtgtgc aggaaccggg 750  
ctcaaggcct cgtttccttc tggggcctct ggtggggcga ccccaagacc 800  
cccgactgtt acacgcaggt gtcgcctttt gtggcctgga tctgggacgt 850  
ggttcggggg agcagtcccc agcccggccc cctgcctggg accaccaggc 900

cccaggaga agcgcgcctga gccacaaact tggggatga aatgagatg 950  
 ggcgcgcag gcctggaatg ttccgtgggt gggcccccag ggaagcctga 1000  
 tggtcagggg tgggggtggga cgggcagcgg tggggccacac ccattccaca 1050  
 tgcacagggc agaagcaaac ccagtaaaat gtttaactgac aaaaaaaaaa 1100  
 aaaaaaaaaa gaaa 1114

<210> 111  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
 Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
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 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
 20 25 30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
 35 40 45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
 50 55 60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
 65 70 75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
 80 85 90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
 95 100 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
 110 115 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
 125 130 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
 140 145 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
 155 160 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
 170 175 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
 185 190 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

204	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg		
215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly		
230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val		
245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly		
260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala		
275	280	

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaagtcagca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

agagaagqaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgaacattac catgctctgc accgcagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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cctgaagcct gacgcctgtc cccggcccgg catgagccgc tacctgttgc 100  
cgctgtcggc gctgggcaag gttagcaggcg ccgcctgtct gctcaaggac 150  
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200  
ggtcacctgt acggggcgca acacaggcat cgggaagcag accgccttgg 250  
aaatggccag gagaggaggg aacatcatcc tggcctgcgc agacatggag 300  
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cggcacctgg acttgggttc cctcaagtct atccgagagt 400  
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aacgggggtg tgatgggtg ccccactgg accacggagg acggcttoga 500  
gatgcagttt gggttaaac acctgggtca cttctctttg aaaaacttgc 550  
tgttggaaca gctgaaagcc tcagcccttt cggggtatcat caacctctcg 600  
tccttggccc atgttgtgtg gcacatagac tttagcact tgaactggca 650  
gacgaggaag tataacacca aagccgccta ctgcagagc aagctcgcca 700  
tgtctcttt caacaaggag ctgagccggc ggttgcaagg ctctggtgtg 750  
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cacgggcata catggctcca cttctccag caccacactc gggcccatct 850  
cttggctgtc ggtcaagagc ccgagctgg ccggccagcc cagcacatac 900  
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actcaaacag aaggccccgg ccccagaggg tgaggatgag gaggtggccc 1000  
ggaggctttg ggtgaaagt gccgccttgg tgggcttaga ggctccctct 1050  
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gcctgtcggg gagggttcca aggtgtccg tgaagagcat gggcaagttg 1450

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 ctgtctccca tgatgggttg gtacagcgag ctgtgtcttg gctatggcat 1600  
 ggtgtgctg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650  
 gagagcaggt gcaggtgtca tcccgagttc aggcctctga cggcatggag 1700  
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggaactc 1750  
 cacttcccta tcaattctca tggtagtcca aactgcagac tctcaactt 1800  
 gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
				20					25					30

Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35					40					45

Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
				50					55					60

Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
				65					70					75

Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80					85					90

Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95					100					105

Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile
				110					115					120

Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125					130					135

Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140					145					150

Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala
				155					160					165

Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170					175					180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				135					191					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttogcg agogctggca tgtggtcctg gggcggggt ggogggogtg 50  
 ctggcggtgc tggcgctogg gacaggagac ccagaaaagg ctggcgctcg 100  
 gggcgacacg ttctggggc tgaccagcgt ggocggcgcc ctggcgcccg 150  
 agcgccgggt gctggggctg ctgaggcggt aactggcggg ggaggaggcg 200  
 oggtcggggg aactgactag attctaagac aaggtacttt ctttgcattga 250  
 ggattcaaca aacctgtgg ctaacctct gcttgcatth actctcatca 300  
 aacgootgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggccctg atggcgctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
agagtcaatg gctctgcaat caatgacctg tacagcccca aacggctctt 550  
ttctctcaca ggggatgaat gattccaagt tggcaaggty gcttatgaca 600  
tggtggatta ttacatgac attccatggc tggaggaggc tgtcagtctc 650  
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700  
agatgctctg gatcaattgg cctttgotta ttccgggcca ggaaatgttt 750  
cgtgtgacct cagctctctt cgggagtttc ttctctacag ccagataat 800  
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
ccccaaccac gtggtagctg aggtctgcat ccagaggccc aatatacccc 900  
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
cagccactc totaaccagat ccttagcttc tactgttctt atgagaccaa 1000  
ttccaacgac tactgtctgc tccagcccat ccggaaggag gtcacccacc 1050  
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cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggtygc 1150  
atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
ggctgaagga cactgttgac ccaaaactgg tgacccctca caccgcatt 1250  
gctgcctca caggccttga tgtccggcct ccttatgcag agtatctgca 1300  
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acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
actgaactgt tggcagagag aagctggtyg agtctgttyg ctttcagag 1700  
aagccaggag ccaaaagctg gggtaggaga ggagaaagca gacagcctc 1750  
ctggaagaag gcttgtcag ctttgtctgt gctcgcaaa tcagaggcaa 1800  
gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcacc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtyga 1900  
 ggccagagag ggaagttttt ggagttcaga tactctctgt tgggaacagg 1950  
 acatctcaac agtctcaggt cagatcagtg ggtcttttgg cactttgaac 2000  
 ctgaccaca gggaccaaga agtggcaata agpacacctg caggagggggc 2050  
 tagcctgact ccagaaactt taagaatttc tcccactgc cttctgtgc 2100  
 agcccaagca gggagtgttc cctccacaga agcatatccc agatgagtgg 2150  
 tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200  
 tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

\*210\* 118  
 \*211\* 544  
 \*212\* PRT  
 \*213\* Homo sapiens

\*400\* 118  
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala  
 1 5 10 15  
 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr  
 20 25 30  
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg  
 35 40 45  
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala  
 50 55 60  
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu  
 65 70 75  
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe  
 80 85 90  
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His  
 95 100 105  
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr  
 110 115 120  
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly  
 125 130 135  
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn  
 140 145 150  
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser  
 155 160 165  
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr  
 170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser  
530 535 540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

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<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

gggcaagtga tccaaggcat ctts 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgaggggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<433> 122

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tccaccctt aggaagccac cagaactcac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggttg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taacccgggc ggggagcgcc caggatgcg 200  
cgcggggaat cggagcaggt gcgtactgc gggcgcttct cctacctctg 250  
gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcaccc tcatcctct 400  
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ctcactatgg agctcattgg tggcgtgggt gccttgacct ccgggaacca 550  
gaccattgac tctctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggaactcaaa aacatcatgg accttgttca gaaaaagttc 650  
aagtgtgtg ggggggagga ctaccgagat tggagcaaga atcagtacca 700  
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<210> 123

<211> 294

<212> FRT

<213> Homo sapiens

<400> 123

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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
		20							25					30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
			35						40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
			50						55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
			65						70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
			80						85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
			95						100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
			110						115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
			125						130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
			140						145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
			155						160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn			
	185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val			
	200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile			
	215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly			
	230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr			
	245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp			
	260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly			
	275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn			
	290		

<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

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<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagatgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtctgtg ggcattatg cagaggttga gggcagaaa tataaaacc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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gtgcccctct gacacctggg aagatggcg gcccgaggac cttacacctt 100

ctctgtgggt tgcctggcag cactctgac caagccacc tcagtccac 150

tgcagttctc atctctgggc caaaagtcac caagaaaag ctgacacagg 200

agctgaagga ccacaaagg accagcacc tgcagcagct gccgtgtct 250

agtgcacatg gggaaaagg agccggagg atccctgtgc tgggcagcct 300

ggtgaacacc gtctgaagc acatcatct gctgaaggtc atcacagcta 350

acatctcca gctgcaggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc cctggacat ggtggctgga ttcacacgc cctggtcac 450

gaccatcgtg gagtccaca tgcagactga ggcacaagg accatccga 500

tggacaccag tgcagtggc cccaccgcc tggctctcag tgaactgtgc 550

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accaagtgtt tcaataactc tgcagcttcc ctgacaatgc ccacctgga 900

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cacctgggc atcgaagcca gctcgggaag tcagttttac accaaagggt 1250

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 atgaactctg ggattggctg gttccaaact gatgttctga aaaacatcat 1350  
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<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128  
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 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170	175	180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu	185	190	195
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly	200	205	210
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu	215	220	225
Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys	230	235	240
Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser	245	250	255
Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu	260	265	270
Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser	275	280	285
Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu	290	295	300
Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His	305	310	315
Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp	320	325	330
Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr	335	340	345
Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu	350	355	360
Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu	365	370	375
Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr	380	385	390
Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp	395	400	405
Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp	410	415	420
Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu	425	430	435
Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu	440	445	450
Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys			

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
 470 475 480

Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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 aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
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gtatattttg tattacctct ttttttcaag tgattttaat agttaatcat 1150  
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 aactactact ttgttttagt tagaaccaaag ctcaaaaacta ctttagttaa 1350  
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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 150

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Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln

	20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met	35	40	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys	50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile	65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys	80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg	95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp	110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser	125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg	140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln	155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val	170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu	185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met	200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys	215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg	230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn	245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His	260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu	275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys	290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

305

310

315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr  
 320 325 330

Ser Phe Leu Met Ser  
 335

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 tcagaacgca tacggcgcat gctactgctg tgggtgtcgg tggtcgcaga 150  
 cttggcgctg ggggtactgg ccccgaggag aggggagcag agggcgagag 200  
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattccag aagtcaggta gtgaaacttc cttttatcaa 300  
 ctttatgaag acacgtggga cttcccttct gaatgcctac acaaacctctc 350  
 caatttgctg cccattccgc gcagcaatgt ggagtggcct cttcactcac 400  
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 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750  
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gcattgtacga ggcctagtcca catgttccgc ttttgatgat gggaccagga 1150  
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ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250  
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ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550  
cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaaagt 1600  
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650  
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750  
ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800  
atgaaacagt ttttaataatt accaagtttt ggcggggcac agtgggtcac 1850  
acctgtaac ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900  
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agtgaagtga gattgcgcca ctgtactcca gctggccaac agagtgagac 2100  
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
tattttgtaa gaatgtagtg tattttaaga taaaatgcc atgattataa 2200  
aatccatat ttccaaaaat ggthattatt taggcctttg tacaatttct 2250  
aaccaatttag tggaagtac aaaaggattg aagcaaatac tgtaacagtt 2300  
atgttctttt aaataataga gaatataaaa tattgtaata atatgtatca 2350  
taaaatagtt gtatgtgagc atttgatggg gaaaaaaaaa aaaaaaaaaa 2400  
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<010> 132  
 <011> 536  
 <012> FRT  
 <013> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala	1	5	10	15
Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	20	25	30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	35	40	45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	50	55	60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	65	70	75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	80	85	90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	95	100	105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	110	115	120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	125	130	135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	140	145	150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	155	160	165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	170	175	180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	185	190	195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	200	205	210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	215	220	225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	230	235	240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	245	250	255	

Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	260	265	270
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	275	280	285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	290	295	300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	305	310	315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	320	325	330
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	335	340	345
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	350	355	360
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	365	370	375
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Glu	Thr	Phe	Lys	380	385	390
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser	395	400	405
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg	410	415	420
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile	425	430	435
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr	440	445	450
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln	455	460	465
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val	470	475	480
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile	485	490	495
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln	500	505	510
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln	515	520	525
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val					530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
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tcaaggagca agagcttcag cctgaagaca agggagcagt cctgaagac 100  
gtttctactg agaggctctg catggactct cttggcctcc aacttgtggg 150  
ctacatccta ggccttctgg ggccttttggg cacactgggt gccatgctgc 200  
tccccagctg gaaaaacaagt tcttatgtcg gtgcacagcat tgtgacagca 250  
gttggtcttct ccaagggcct ctggatggaa tgtgcacac acagcacagg 300  
catcacccag tgtgacatct atagcacctt tctgggcctg cctgctgaca 350  
tcaggcttgc ccaggccatg atgggtgacat ccagtgcatt ctctccctg 400  
gcctgacatta tctctgttgt gggcatgaga tgcacagtct tctgcacagga 450  
atccccagcc aaagacagag tggcggttagc aggtggagtc ttttccatcc 500  
ttggaggcct cctgggattc attcctgttg cctgggaatct tcattgggac 550  
ctacgggaact tctactcacc actggtgcct gacagcatga aatttgagat 600  
tggagaggct ctttacttgg gcattatttc ttcctgttc tcctgatag 650  
ctggaatcat cctctgtttt tctgtctcat ccagagaaa tcgtcccaac 700  
tactacgatg cctaccaagg ccaacctctt gccacaagga gctctccaag 750  
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cagggctatgt gtgaagaacc agggggcaga gctgggggggt ggcctgggtct 850  
gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900  
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
attgccaagg atgctcgcca tgcacgctt tctgttttcc tcaccttgc 1050  
gctcccttgc cctaagtccc caacctcaa cttgaaaacc cattccctta 1100  
agccaggact cagaggatcc ctttgcctc tggtttacct gggactccat 1150  
ccccaaaacc actaatcaca tccactgac tgacctctg tgatcaaaga 1200  
cctctctctt ggcctgaggtt ggccttttagc tcattgctgg ggatgggaag 1250  
gagaagcagt ggccttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccttggaaac ttcattccac tcttggttatg 1351  
 aatccacagt gtccagarta atttgtgcac gaactgaaat aaaaccatcc 1400  
 taaggatccc aggggaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
 20 25 30  
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly  
 50 55 60  
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala  
 65 70 75  
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile  
 80 85 90  
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr  
 95 100 105  
 Val Phe Cys Gln Gln Ser Arg Ala Lys Asp Arg Val Ala Val Ala  
 110 115 120  
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro  
 125 130 135  
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro  
 140 145 150  
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr  
 155 160 165  
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile  
 170 175 180  
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr  
 185 190 195  
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg  
 200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 221 225

Leu Thr Gly Tyr Val  
 230

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
 gcaatgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50  
 ctctgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100  
 aagtcatcgc tcccgtcggc tcagaacctt ggcctgtgcca gccggcaccc 150  
 aggtgtggag acaagatcta caaccccttg gagcagtgtt gttacaatga 200  
 cgcacatcgtg tccctgagcg agaaccggca atgtgggtccc cctgcacct 250  
 tctggccctg ctttgagctc tctgtctctg attccttttg cctcacaac 300  
 gattttgttg tgaagctgaa ggttcagggg gtgaattccc agtgcacac 350  
 atctcccatc tccagtaaatt gtgaaagcag aagacgtttt cctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agtccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggttttt caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95						100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
			110						115					

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtcttttgcca tttttctgat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgaactcctt acctgatgct gtgccagcca cacaagagat 150  
 ctgggggacaa gttctaagac cccctgcagc actgtttgcta tgatgatgac 200  
 ctctgtgcctt tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250  
 ctgttttgag cagtgtctgac cctggacctt catggtgaag ctgataaacc 300  
 agaaactgga ctccagcccg accctggatg acaggctttg tcgcagtgtc 350  
 agctaattga acatcagggg aacgatgaat cctggattct ccttctgagg 400  
 tgggccttga gaaagaggct ggtgttaact gagatctggg atgotgagtg 450  
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 accccaagga tggctyggga acccttcacc cttctgtgag attttcacac 700  
 atctcaagtt ctctttctac caggagcaaa gcacaggatc ataataaatt 750  
 catgtacttt ataaatgaaa a 771

<210> 133  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 ctgcgcgcga ccagaaattc ctctgcgcgc ccgacgggga catgggcgctc 150  
 ccacgggcgc tggaggcgcg cagctgggcgc tggggatccc tgcctcttcgc 200  
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 tgcaggctct tgggcctgt ggacaaaggg cagatgtga cctctacaa 350  
 gacgtggtac gcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400  
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 cctgtgtgga tagcgctc tactgctgc tgggtgtgga gatcaggcac 600  
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagctctc gaaagtcacg cctctcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450  
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 ccccgctggc gccttggctc ccccgctttg cccgaggctg ctctctctgc 1550  
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 ctggccatcg ccaccttccc cagctgctc ctaccagcag tttctctgaa 1650  
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 gttgcaccac ccactggaga tggctgtgag ggaggtgggt ggggccttct 1850  
 gggaaaggtg gtggagaggg gcacctgcc ccgcacctcc cctccctca 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgcacac aatgtcttgt 1950  
 ccacctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	
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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

275

280

285

Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp  
290 295 300

Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile  
305 310

<210> 141  
<211> 1732  
<212> DNA  
<213> Homo sapiens

<400> 141  
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cctagacctc ccttctgtgc ctctttctct gccacacgct gcttctgtgc 150  
ccttctccga ccccgctctc gcagcagacc tctgtgggtc tgtgggttga 200  
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ggcccaacca aagtcctgac agcacaaagg gacctgtac caacacggag 650  
agatcttcag tgcccatgag ctgttccctt ccgctctgac caaccagtgt 700  
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cccggaacca ggtgcctcag caccctccc actgcacagc tctgctgac 800  
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
cagtcctcc atgggggtgag acatctcag gatccatgtt ccagtgtgc 900  
tgggagaaaag agaggcccggt gcaccccagc ccccactgga ctacggccc 950  
ctctgagctt catcctctgc cacttcagac ccaagggagc aggcagcaca 1000  
actgtcaaga tcttctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
cgggaagaag tactcccaag gggaggtgtg gcacccggcc ttccgtgctt 1100

tagggccctt gccctgcctc ctatgcacct gtgaggatgg ccggccaggac 1150  
 tggagaggtg tgacctgtcc caccgagtag cccctgcctc accccgagaa 1200  
 agtggctggg aagtgtgtga agatttgccc agaggacaaa gcagacctg 1250  
 gccacagtga gatcagttct accaggtgtc ccaaggccacc gggccgggtc 1300  
 ctgttcacaa catcgttctc cccaagccca gacaacctgc gtcgttttgc 1350  
 cctggaacac gaggcctcgg acttggttga gatctacctc tggaagctgg 1400  
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 ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500  
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550  
 gaaggtcact ggaacgtctt cctagcccag acctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
 gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700  
 catracctc aaaaaaaaaa aaaaaaaaaa aa 1732

«210» 142

«211» 451

«212» PRT

«213» Homo sapiens

«400» 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	290	295	300
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	305	310	315
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	320	325	330
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	335	340	345
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	350	355	360
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	365	370	375
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	380	385	390
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro  
410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala  
425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys  
440 445 450

Thr

<210> 143  
<211> 693  
<212> DNA  
<213> Homo sapiens

<400> 143  
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cttggggaaa atgctgatct cagtgcgaat gctggggcgca ggggctggcg 150  
tgggctaagg gctcctcggt atcgtgaccc cgggagagcg ggggaagcag 200  
gaaatgctaa aggagatgoc actgcaggac ccaaggagca gggaggaggc 250  
ggccagggac cagcagctat tggcggccac tctgcaggag gcagcgacca 300  
cgcaggagaa cgtggcctgg aggaagaact ggatgggttg cggcgaaggc 350  
ggcgcagcgg ggaggtcacc gtgagacggg acttgcctcc gtggggcgccg 400  
gaacttggtc tggggcgagg aatccgaggc agcctttctc cttcgtgggc 450  
ccagcggaga gtcgggacgg agataccatg ccaggactct cgggggtcct 500  
gtgagctgoc gtcgggtgag cacttttccc ccaaacctg gactgactgc 550  
tttaaggctc gcaaggcggg ccagggcgga gacgcgagtc ggatgtggtg 600  
aaatgaaaga accaataaaa tcctgttctt ccaaaaaaaaaa aaaaaaaaaa 650  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
<211> 93  
<212> FFT  
<213> Homo sapiens

<400> 144  
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
1 5 10 15  
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90

Arg Ser Pro

<210> 145  
 <211> 1383  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 ttgaggggaa gaggttgact gtacgttctt tetactctgg caccactctc 100  
 cagggtgcca tgggggcccag caccctctct ctcctcttctg tctttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttggt gactacatgg 200  
 aacgcggact agtggtttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgtgtgtga gctgctggac ttcaagaaca agatgtgtgc 300  
 actgtctggag gtggcagaga aggagcggga ggcactcaga actgagggcg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400  
 gagaccaga accagctctt ggcctgtgta gagtttgatg agaaggtgac 450  
 tggaggccct gggaccaaa gcaagggaag aaggaatgag aagtaagata 500  
 tggtagacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctgggtct tggaccaagg atccactggg 600  
 gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650  
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 gcttcccgag tccgggtgct cttcccttgg gtaggcacag ggcagctggt 750  
 atatggtggc tttcttttatt ttgtcggag gctccttgga agactgggtg 800  
 gaggtggtga gatggagaac actttgcagc taatcaaat ccacctggca 850  
 aacccaacag tggtagacag ctccagtatt ccaggagagg ggtgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gatgatgagg 950  
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcctc tgtgggaccc 1100  
 totatgttgt ctataacacc cgtcctgcca gtggggcccg cctccagtgc 1150  
 tcttttgatg ccagcggcac cctgacccct gaacgggcag cactccctta 1200  
 ttttccccgc agatatggtg cccatgccag cctccgtat aacccccgag 1250  
 aaagccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
 catctttctc actcccatac atttatatta tatcccaact aaattttctg 1400  
 ttctccttcc ttcacatgtg ggccagttgt ggcctcaaat ctctatattt 1450  
 ttagccaatg gcaatcaaat tctttcagct cttttgtttc atacggaact 1500  
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
 ttccctcctg ctctcctgcc ccattgtcaac aaatttcagg ctaaggatgc 1600  
 ccagaccca gggctctaac cttgtatgag ggcaggcca gggagcaggc 1650  
 agcagtgttc ttccctcag agtgaattgg ggaggagaa ataggaggag 1700  
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750  
 aacaggactt totccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PPT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala					
				65					70					75					
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu					
				80					85					90					
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro					
				95					100					105					
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys					
				110					115					120					
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys					
				125					130					135					
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg					
				140					145					150					
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln					
				155					160					165					
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala					
				170					175					180					
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala					
				185					190					195					
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr					
				200					205					210					
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro					
				215					220					225					
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln					
				230					235					240					
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser					
				245					250					255					
Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala					
				260					265					270					
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala					
				275					280					285					
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys					
				290					295					300					
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro					
				305					310					315					
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr					
				320					325					330					
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile					

335

340

345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
395 400 405

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50

cagctcaccg agagcctctc cgtggcttcc gcaccttgag cattaggcca 100

gttctcctct tctctctaat ccctccgtca cctctcctgt cctccgtttc 150

cctgcctgtg ggctccatca cagaacacat ccctggctct cctgctcagt 200

ctggctctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250

gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctct 300

gttctcgtgc tcttaagacc aatgcagagg ccctgggaagt gcggttcttc 350

agggggccagt tctctagcgt ggctccctc tacagggaag ggaaggacca 400

gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450

attctattgc ggaggggcgc atctctctga ggttggaaaa cattaactgt 500

ttggatgctg gcctctatgg gtgcaggatt agttccagct cttactacca 550

gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600

tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagttc 650

tgggctggt tccccgggc cacagogaag tggaaaggtc cacaaggaca 700

ggatttgtcc acagactcca ggacaaacag agaatgcct ggctgtttg 750

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tccatgggc atgctcatct gaggcagag gtggaatcca ggttacagat 850

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 ttctttctca aattccagtg gaaaatccag ggggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc cgggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gtcacccga agctctgggt ttctgatctg 1100  
 aaaactgtaa ccataaaaa agctcccccag gagggtgctc actctgagaa 1150  
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 cattaatacc cgtttttatc agcgtcttcc ccaggacccc acctacaaaa 1400  
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aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

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Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val Gln	Ala 30
20	25		
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser Pro	Lys 45
35	40		
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly Gln	Phe 60
50	55		
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln Pro	Phe 75
65	70		
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val Lys	Asp 90
80	85		
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn Ile	Thr 105
95	100		
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser Gln	Ser 120
110	115		
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala Leu	Gly 135
125	130		
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg Asp	Ile 150
140	145		
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro Thr	Ala 165
155	160		
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp Ser	Arg 180
170	175		
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile Ser	Leu 195
185	190		
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met Arg	His 210
200	205		
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile Gly	Asp 225
215	220		
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys Val	Leu 240
230	235		
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu	Lys 255
245	250		
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu	Asp 270
260	265		
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys 285
275	280		
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys

290	295	300
Leu Cys Val Ser Asp 305	Leu Lys Thr Val Thr His Arg Lys Ala Pro 310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val 320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val 335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp 350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His 365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr 380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr 395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe 410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg 425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn 440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu 455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu 470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu 485	490	495
Pro Arg Gly Glu Met 500		

<310> 149

<311> 24

<312> DNA

<313> Artificial Sequence

<320>

<323> Synthetic oligonucleotide probe

<400> 149

gggtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 150  
ggaaatgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 151  
gcagatgaca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
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aatgaatggc ggagccgggc ggcgcctgag gagcctggcg agcctggggc 150  
gcctggccct gttgtgtgc gccgcggcgc ccgcggccgt cgcctcagcc 200  
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cgcgctggcc ggcccggggt tgggggggga gccagaccac cccttcctta 300  
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agaccacagg gcagtgtgan tctcggccag gttatcaggg gcttcactgt 800

gaaaactgca aagaggggctt ttacttaaat tacactcttg ggtctgtca 850  
 gccatgtgac tgtagtccac atggagctct cagcatacag tgcaacaggt 900  
 aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950  
 aaaaggctgc tactotcaag gaccatactg gtttaaacaa aggaggatga 1000  
 gggcataga tttaaaaaat attttatata cttttattct cttactttat 1050  
 atgttatatt taatgtcagg atttaaaaaa atctaattta ctgatttagt 1100  
 tottcaaaag caatagagtc gccaattttt ctctgggata attctgttaa 1150  
 atttcacggg aaaaaattat tgaagaataa atctgttttc tggaagggct 1200  
 ttcaggcatg aaactgtcta ggaggtttag aaatgttctt atgtttatta 1250  
 atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
 taatcaaaat totacatttg tttctttgga catctaaagc ttaactggg 1350  
 ggtacccata tttattttaac tagtggtaag tagactgggt ttactctatt 1400  
 taaccgtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
 aactattatg ttatttgag gtaatttaac ctagtgggat aatgtactgt 1500  
 tatctaagca tttgccttgc actgcactga aagtaattat totttgaact 1550  
 tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600  
 acagtattaa ataatgaaaa aaataatgac aggttatact cagtgtaac 1650  
 tgggtataac ccaagatctg ctgcccacta cgagctgtgt tcttgggca 1700  
 agtaatttcc tttcactgag cttgtttctt ctcaagggtg ttgtgaagat 1750  
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 ctgggttctt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850  
 tgttttaaga acttttagct ccttgacaaa gaagtgttct atacttttagc 1900  
 actaaatatt ttaaactgct tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgggggg 2000  
 ctcaagcctg taatcctago actttgggag gccaaaggcg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aacccgtct 2100  
 ctactaaaaa tacaaacaaa ttagctgggc gtgggtggcc acacctgtag 2150  
 tcccagctac tggggaggtt gaggcaggag aatcggttga accggggagg 2200

aggaggttgc agtgagctga gatcgagcca ctgcactcca gcttggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15

Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro  
 245 250 255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<401> 154  
 aactgctctg tgggtggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgggggcag tgtagaacctg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcttt ggtctcgggtg ccacagggccc aggcctgtgtg gttgggaaga 100  
 ctggacctgt agcagcttct tgggccttgg tacgtgcttg cgggtggcctc 150  
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200  
 tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtctctcag 250  
 caccggctgg gaggggtgtg ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggggtgtg gagctctggg 350  
 tggctggccac caacttcaga gactatgcca tcatcttcaa ttagctggag 400  
 ttgggggacg agcccttcaa caccgtggag ctgtacagtc tgaaggagac 450  
 agccagccag gaggccatgg ggcctctcac caagtggagc aggagcctgg 500  
 gcttctgttc acagtacagc gccagctgc agaaggacct cactgtgtct 550  
 cacaagatcc ttctgtgagt gctggctccc cagtagggat gggtccaca 600  
 gggctctgtg acctgggcca gtgtccacc acctcgctca gggctcccg 650  
 gggccacaga ccagctcaga ataaagcgt tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90  
 Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
 95 100 105  
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
 110 115 120  
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
 125 130 135  
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
 140 145 150  
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln  
 155 160

<210> 159

<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159

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gctgctgctg cccctgctct gggggaggga gagggggga ggacagacaa 100  
gtaaaactgt gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
gtccatgtgc cctgctcctt cctctacccc tcgcctgggt ggatttcccc 200  
tggcccagta gttcatgggt actgggttcg ggaagggggc aatacagacc 250  
aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaggag 300  
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcctc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacagggcc aacatctca tcccaggcac 500  
cctggagtcc ggtgccccc agaactgac ctgctctgtg cctggggcct 550  
gtgagcaggg gacacccct atgatctct ggataggga ctcctgtctc 600  
ccctgggacc cctccaccac ccgtcctctg gtgctcacc tcatccaca 650  
gccccaggac catggcacc gctcaccctg ccaggtgacc tccctgggg 700  
ccagcgtgac caggaacaag accgtccctc tcaacgtgtc ctacccgct 750  
cagaacttga ccctgactgt ctcccaagga gacggcacag tatccacagt 800  
cttgggaaat ggtctatctc tgtcactccc agagggccag tctctggccc 850  
tggtctgtgc agttgatgca gttgacagca atcccccctg caggctgagc 900  
ctgagctgga gaggcctgac cctgtgcacc tccacagcct caaacccggg 950  
gggtctggag ctgccttggg tgcacctgag ggtatgcagt gaattccct 1000  
gcagagctca gaacctctc ggtctcagg aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtgaat caggggggtg tcgggggagc 1100  
tgagaccaca gccctggtct tctgtcctt ctgcgtcctc ttggtttag 1150  
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcctag aggatgcaaa cgtgtcagg ggttcagcct ctccggggcc 1250  
cctgactgaa ccttgggcag aagacagtc ccacagaccg cctccccag 1300

ctcttgcccg ctcttcagtg ggggaaggag agctccagta tgcctccctc 1350  
 agcttcacaga tgggtgaagcc ttgggaactcg cggggacagg agggcactga 1400  
 caccgagtag cgggagatca agatccacag atgagaaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacy tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
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 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Hcmo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	110	115	120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	125	130	135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	140	145	150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	155	160	165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	170	175	180	

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala	410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser	425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu	440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg	455	460	

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgcaga ggtcggcaga acagagctct ggagatgaag 50  
 acctgttcc tgggtgtcac gctcggactg gcgctgccc tgtccttcac 100  
 cctggaggag gaggatata cagggacctg gtacgtgaag gccatggtgg 150  
 togataagga ctttcggag gacaggaggc ccaggaaggt gtcccagtg 200  
 aaggtgacag cctcgggcgg tgggaagttg gaagccact tcaccttcac 250  
 gagcgaggat cgggtgcacc agaagaaaat cctgatggcg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgccc ggagggacca ctacatcttt tactgcaaag accagcacc 400  
 tgggggctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcacca 550  
 acactaggca gccccgggt ctgcacctcc agagccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650  
 gctccaccac acctgacct aaataaagtc cttttccccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
 20 25 30  
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
 35 40 45  
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
 50 55 60  
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
 65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr  
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro  
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly  
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr  
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys  
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser  
155 160 165

Cys Val Pro Glu His  
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcttcggga aagtccttat c 21

<210> 166

<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gactagtgtt cgggaacgca gcttc 25

<210> 167  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
cagggacctg gtaagtgaag gccatggtgg tcgataagga ctttcggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
ctgtcttcca ccttggagga ggaggatata acagggaact ggtac 45

<210> 169  
<211> 1104  
<212> DNA  
<213> Homo sapiens

<400> 169  
gttcgcgaga tgcagaggtt gaggtggctg cgggactgga agtcacggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100  
aggccatgag gattctgcag ttaactctgc ttgctctggc aacagggtt 150  
gtagggggag agaccaggat catcaagggg ttgagtgca agctcactc 200  
ccajccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250  
cgagctcat cgcgccca ga tggctctga cagcagccca ctgctcaag 300  
cccgctaca tagtcaact ggggcagcac aacctcaga aggaggagg 350  
cttgagagag acccggacag ccactgagtc ctccccccac ccggcttca 400  
acaacagctt ccccaacaaa gaccacgca atgacatcat gctggtgaag 450  
atggcctgca cagtctcat cactgggtgt gtgcagcccc tcacctctc 500

ctacagctgt gtcaactgtg gacacagctg cctcatttcc ggctggggga 550  
 gcaagtccag cccccagtta ggcctggctc acacattggg atgggcgaac 600  
 atcaccatca ttgagcacca gaagtgtgag aagcctacc ccggaacat 650  
 cacagacacc atggtgtgtg ccagcgtgca ggaaggaggc aaggactcct 700  
 gccagggtga ctccggggggc cctctggtct gtaaccagtc tcttcaagga 750  
 attatctcct ggggcacaga tccctgtgag atcaccagaa agcctgtgtg 800  
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 acaattagac tggaccacac caccacagcc catcacctc catttccact 900  
 tgggtgtttgg ttctgttca ctctgttaat aagaaacct aagccaagac 950  
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100  
 tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15  
 Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro  
 20 25 30  
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu  
 35 40 45  
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala  
 50 55 60  
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 65 70 75  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr  
 80 85 90  
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys  
 95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

gggtggggga ctggaagtcg tgggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

cttttggtct gtaaccag 18

<210> 174

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tttttgatgt tgcgggggta ggcg 24

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

cggtgtagaca ccaggctttc ggggtg 25

<210> 176

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

cccttgatga tcttggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 177

agggcatgag gattctgag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gagagaccag gacatcaag ggttccaggt gcaagccca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

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Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60
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Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	185	190	195
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013 Homo sapiens

420 188

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• 111 • 74

• 212 • PRT

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 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
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<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
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				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
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<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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                   20                  25                  30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35										40					45				
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro					
				50					55					60					
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg					
				65					70					75					
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu					
				80					85					90					
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe					
				95					100					105					
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys					
				110					115					120					
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu					
				125					130					135					
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg					
				140					145					150					
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp					
				155					160					165					
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu					
				170					175					180					
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg					
				185					190					195					
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu					
				200					205					210					
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp					
				215					220					225					
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr					
				230					235					240					
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp					
				245					250					255					
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro					
				260					265					270					
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr					
				275					280					285					
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu					
				290					295					300					
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu					
				305					310					315					
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr					

				320						325					330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	
				335					340					345	
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	
				350					355					360	
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	
				365					370					375	
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	
				380					385					390	
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	
				395					400					405	
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	
				410					415					420	
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	
				425					430					435	
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	
				440					445					450	
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser	
				455					460					465	
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser	
				470					475					480	
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe	
				485					490					495	
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg	
				500					505					510	
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg	
				515					520					525	
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn	
				530					535					540	
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys	
				545					550					555	
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys	
				560					565					570	
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu	
				575					580					585	
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val	
				590					595					600	
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn	

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Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser		
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr		
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu		
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly		
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys		
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala		
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln		
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val		
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met		
740	745	750
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr		
755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile		
770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe		
785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg		
800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu		
815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu		
830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly		
845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu		
860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser		
875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr		

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala		
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr		
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr		
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile		
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser		
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly		
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys		
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys		
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile		
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys		
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
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Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
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Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
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Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
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Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
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Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
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Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
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Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

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Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln			
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Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln			
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Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu			
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Glu Cys Gly Cys Leu Ala Cys Ser			
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<111> 14

<112> DNA

<113> Artificial Sequence

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<121> Synthetic oligonucleotide probe

<400> 199

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<110> 200

<111> 14

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 200

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<110> 201

<111> 50

<112> DNA

<113> Artificial Sequence

<120>

<121> Synthetic oligonucleotide probe

<400> 201

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<111> 793

<112> DNA

<113> Homo sapiens

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 gagggaaaat taagctatc ttttaagaaa ataatattt ccatttaa 750  
 gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
 20 25 30  
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 35 40 45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
 50 55 60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
 65 70 75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
 80 85 90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
 95 100 105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
 110 115 120

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 131 136

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 146

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

ggcagctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcttggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtgaggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgcacca aggcctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<213> Synthetic oligonucleotide probe

<410> 209

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<410> 209

caggccattt gcacccact gtccctgtgt tcggagccag gccacacgt 50

cctcagcagt gtcctgtgtt aaaaacgcc aactgaatat atcatgcacc 100

tattaaaaact tgtacatggc tcccattgg tttttggaga aaagttcaag 150

ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

ggggaagaag atccatattt actgtcactt ccagatctg cttctcacca 250

agagagattc tttctttaa cgaactataa gggccccaat tgaactggata 300

gaggaatata ccacagggat ggcagaactg atcttagtca acagccagtt 350

ccagctgtct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400

ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcaagttgtt 450

cctgaaaagc tggatgaact agtccccaag gggaaaaaat cctgtgtgtct 500

ctccatcaac agatacgaac ggaagaaaaa ctgactttg gcaactggaag 550

ccctagtaca gctgcttgga agattgaact cccaagattg ggagagggtt 600

catctgatcg tggcaggtgg ttatgacgag agagtcttgg agaattgtga 650

acattatcag gaattgaaga aaatgggtca acagtccgac cttggccagt 700

atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctctct 750

ccagctgca cgtgtgtgtct ttacacacca agcaatgagc actttggcat 800

tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850

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gagcctgacc cggtgcactt ctcaagaaca atagaaaagt tcatccgtga 950

accttcttta aaagccacca tgggcttggc tgggaagagcc agagtgaagg 1000

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aaactgtctg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100

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 tgcattcca tgttcagcag agtattttaa ctatattttc tggggattat 1350  
 tgcctctctg ctatataaatt ttgaatgata ctgtgcctta attgggtttc 1400  
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 ataattgagag cagggctatt gtatgtccca gattcaatcc accgaagtgt 1500  
 tcactgtcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaagggt gtttatcata aaaaaaaaaa aaaaaaaaa 1643

2100 210  
 211 323  
 212 PRT  
 213 Homo sapiens

400 210  
 Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly  
 1 5 10 15  
 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val  
 20 25 30  
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His  
 35 40 45  
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg  
 50 55 60  
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly  
 65 70 75  
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val  
 80 85 90  
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val  
 95 100 105  
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro  
 110 115 120  
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu  
 125 130 135  
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala  
 140 145 150  
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg		
170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val		
185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe		
200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val		
215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu		
230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly		
245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu		
260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg		
275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg		
290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr		
305	310	315
Arg Tyr Val Thr Lys Leu Leu Val		
320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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cttcgggagc ttgcgcgtta cctttcttgc ggcgttggtg ggagccgtgc 100

tctacctcta tcgggtctcc agacaagctg caggaattcc agggattact 150

ccaactgaag aaaaagatgg taattcttcc gatattgtga atagtggag 200

tttgcattgag ttccctggta atttgcattg gagatatggg cctgtggtct 250

cctttctggt ttgcaggcgc ctgcgtggtta gtttgggcac tgttgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaattctg tggtaggcagt gtgagtgaag 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg cctctctctt aaagctttca gaagaattat tagataaatg 500  
 gctctctctac ccagagaccc agcactgccc cctcagcccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cactctgaa gaagtccaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tctgttact ccagagaaaa 1000  
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaaactga ctccagtttc tgcacagctt caagatattg aaggaaaaat 1100  
 tgaacgattt attattccta gagagacct cgtcctttat gcccttggtg 1150  
 tggtaacttca ggatcctaact acttggcact ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct caattggatt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtaacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggtac actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala		20	25	30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu		35	40	45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn		50	55	60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg		65	70	75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His		80	85	90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys		95	100	105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn		110	115	120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu		125	130	135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu		140	145	150
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser		155	160	165
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val		170	175	180
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln		185	190	195
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu		200	205	210
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu		215	220	225
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys		230	235	240
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser		245	250	255
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser		260	265	270
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys		275	280	285
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys		290	295	300

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305					310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320					325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335					340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350					355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365					370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380					385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395					400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410					415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425					430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440					445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455					460						

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
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 tccagctca gagacggcgg ccttggtccc cgaggccat gggccgggtc 100  
 tcagggttg tgcctctcg ctctcgacg ctctggcgc atctggtggt 150  
 cgtcaccacc ttattctggt ccggggacag caacatacag gctgcctgc 200  
 ctctcaggtt caccocggag gagtatgaca agcaggacat tcagctggtg 250  
 ggcgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcctcc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtga ctagtattg gtacatttt gtctcttga gtgccttcc 450

agctgtcaact gaaatgggtt tatctgtcac cgtctttggg ctgaaaaaga 500  
 aacccctctg attaccttca tgaagggaac ctaaggacga agcctacagg 550  
 ggaaggggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600  
 ttccctctgg aaactgcttc tgcctggagga tatgtgttgg aataattacg 650  
 ccttgagctct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tcttttctag taacattaag acttatatac agttttaggg gacaattaaa 750  
 aaaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> FRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45  
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
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 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
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atggggtctt ccccagcttc ctccgactcg gaggggtctc ggagacagaa 100  
 gacccgggctt gctgcagccc catagtgcct cggaaacagt ggaaggccct 150  
 agcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatgcacac ggcgggcagc agctgcaaca ccccgccttc gtgcacagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgga 300  
 cgtgggtctc aacttctga ttggagaaga cgggctctga tacgagggcc 350  
 gtgactggaa ctccacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcct gggcaactac atggatcggg tgcacacacc 450  
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 gagcctgag gtccaaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctacgctcc cctgagggcc ctgctgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctctctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1				5					10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
			20						25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
				35					40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
				50					55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
				65					70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
				80					85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
				95					100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
				110					115					120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
			125						130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
			140						145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
			155						160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
			170						175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
			185						190					195

Pro

<210> 217  
 <211> 1871  
 <212> DNA  
 <213> Homo sapiens

<400> 217  
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 gaagatgcaa ctgactcgct gctgcttcgt gttcttggtg cagggtagcc 100  
 tctatctggt catctgtggc caggatgatg gtctctccgg ctacagaggac 150  
 cctgagcgtg atgaccaaga gggccagccc cggccccggg tgctctggaa 200  
 ggjgggcac atctcaccta agtccccccc catggccaat tccactctcc 250  
 tagggctgct ggccccgctt gggjaggctt ggggcattct tgggcagccc 300  
 cccaaacggc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350  
 ctttggtgg ggagactctt actccaaat caagacgggt gcctgaacc 400  
 tggctgtcac agjgaagatt gtggaccatg gcaatgggac ctccagcgtc 450  
 cacttccaa acaatgcac aggcaggga aacatctcca tcagcctcgt 500  
 gcccccagc aaagctgtag agttccacca ggaacagcag atcttcacgc 550  
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtj ggagaaggta 600  
 gaaaggggcc gcgggacctc gctttgcacc caggaccag ccaagatctg 650  
 ctcccgagac cagctccaga gctcagccac ctggagctgc tcccagccct 700  
 tcaagctcgt ctgtgtctac atgcctctt acagcacgga ctatcggtc 750  
 gtccagaagg tgtgcacaga ttacaactac catagtata cccctacta 800  
 cccatctggg tgacccggg caggccacag aggcagggcc agggctggaa 850

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 gccagggcca agtctcaagt ggcagagaaa ggytcccaag tgcctggccc 1000  
 aacctgaagc tctggagtga ctagatcaca ggagcaactg aggaggagtg 1050  
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 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
 gtcatgggag gaagctaagc ccttggttct tgcctcctg aggaaagata 1200  
 gcaacagggg ggjggagatt tcctcagtgt ggacagcctg tcaacttagg 1250  
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 gccagaggag ctctccagcc ctgcctagtg ggcgccctga gcccttctc 1350  
 gtgtgtgag catggcatga ggctgaagtg gcaacctgg ggtctttgat 1400  
 gtcttgacag attgacctc tctctccagc caggccacc ctttccaaaa 1450  
 ttcctcttc tgcagtact cccctgtac caaccattgc tgatggcaca 1500  
 cccatcotta agctaagaca ggaagattgt ggtctccca cactaaggcc 1550  
 acaccccatc cgggtgtgt gtgtccctct tcaccccaa cccctgtctg 1600  
 ctctctggg agcatccatg tccggagag gggctccca acagtcagcc 1650  
 tcactgtca gacgggggtt ctccggatc tggatgggg cggcctctca 1700  
 gcaacgggca cgggtggggc ggggcggggc cgcagagcat gtgtggatc 1750  
 tgtctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800  
 aacgtgtgat tctgaactt tgtgtgaaga atcgtgtct tggagcagga 1850  
 aataaagctt gccccggggc a 1871

<210> 218  
 <211> 252  
 <212> FRT  
 <213> Homo sapiens

<400> 218  
 Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser  
 1 5 10 15  
 Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
 20 25 30  
 Gln Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
 35 40 45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	215	220	225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	230	235	240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				245	250	

<210> 219  
 <211> 2065  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
 gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50  
 gcagggggccc caggcagggc tgattcttgg gggaggaga gtagggtaaa 100  
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200

gagcgcgcgc gcgcgtcgct cctgcagcgc tctcgaccta gcgcctagca 250  
tcttcacagc caccgggata cgggggtagg aggcgaacgc ggcgagcacc 300  
agcgccagcc ggcctgggct gccacacgg ctccacatgg gctccggggc 350  
ccggggcgctg tcgcgggtgc cggcgtgct gctggctctc acgctgcgg 400  
ggctgcgcgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tgggtgtgca ctgcaacccg gccacggact ccaagggtc 500  
ctcttctctc ccgctgggga tatcggtccg ggcggccaac tccaaggtcg 550  
ccttctcggc ggtgcggagc accaacacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctgggtgaatg tgggtaattt 650  
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccagggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800  
tgttaactcg gaagctgcca cgaatggtgt cctgctctac ctgataaag 850  
aggataaggt ttacctaaaa ctggagaaaag gtaatttggt tggaggctgg 900  
cagtattcca cgtttctctg ctttctggtg ttccccctat aggattcaat 950  
ttctccatga tgttcatcca ggtgagggat gacccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
ggtggatatg gattctaaag attctagcct gtctgaacca atacaaaatt 1100  
tcacagatta tttgtgtgtg tctgtttcag tatatttggc ttgggactct 1150  
aagcagataa tacctatgct taaatgtaac agtcaaaaagc tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
gaaaactcta aagttctgac ttcaatcaac gggttagtgt atactgcaa 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttatttcctt 1400  
ggaattagtt tgtttggtc ttgtaaaaaa cttggatttt ttttttcagt 1450  
aactggtatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500  
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550  
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600  
ccaagttata ttttctaaag agaagaatag atctaatc tgacaaggaa 1650

aaagttggtt acccaaaaatc taagtgtca atccctgagc ctcagcaaaa 1700  
 cagatccctt ccgagggaaa tcttatactt tattgtcaa ctttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaagggtt ttttttttc 1800  
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta ttgaagtat catctgggtt 1900  
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950  
 ttcaaatac ccatatctaa atttagtga atatcttgct tttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgct tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

(210) 220  
 (211) 201  
 (212) PRT  
 (213) Homo sapiens

(400) 220  
 Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
 1 5 10 15  
 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
 20 25 30  
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
 35 40 45  
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
 50 55 60  
 Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
 65 70 75  
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
 80 85 90  
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
 95 100 105  
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
 110 115 120  
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
 125 130 135  
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
 140 145 150  
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
 155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
 170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
 185 190 195

Phe Leu Val Phe Pro Leu  
 200

<210> 221  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 221  
 acgggtcacc atgggctcgg 20

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 aggaagagga gcccttggag tccg 24

<210> 223  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
 cgttctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224  
 <211> 902  
 <212> DNA  
 <213> Homo sapiens

<400> 224  
 cgggtggccat gactgcggcc gtgtttcttcg gctgcgcctt cattgccttc 50  
 gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100  
 tctcatcttc ctcatgcgc gagctttctt ctggttggtg tctctactga 150  
 ttctgtccct tggttggttc atggcaagag tcattattga caacaaagat 200

gaacaaacac agaaatatct gctgatcttt ggagagcttg tctctgtcta 250  
 tatccaagaa atgttcagat ttgcataatta taaactotta aaaaaagcca 300  
 gtgaaggctt gaagagtata aaccacaggtg agacagcacc ctctatgoga 350  
 ctgctggcct atgtttctgg ctggggcttt ggaatcatga gtggagtatt 400  
 ttcctttgtg aataccctat ctgactcctt ggggacagga acagtgggca 450  
 ttcattgaga ttctctcaca ttcttctctt attcagcttt catgacgtg 500  
 gtcattatct tcttgcctgt attctggggc attgtatttt ttgatggctg 550  
 tgagaagaaa aagtggggca tctccttat cgttctctg acccacctg 600  
 tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
 tcagcattta taatcttggg gctcatgggc acctgggcat tcttagctg 700  
 gggaggcagc tgcgaagcc tgaaactctg cctgctctgc caagacaaga 750  
 actttctctt ttacaaccag cgtctcagat aacctcaggg aaccagcact 800  
 tcccaaaccc cagactacat ctttagagga agcacaactg tgcctttttc 850  
 tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
 ta 902

<210> 325  
 <211> 357  
 <212> PRT  
 <213> Homo sapiens

<400> 225  
 Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly  
 1 5 10 15  
 Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu  
 20 25 30  
 Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
 35 40 45  
 Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
 50 55 60  
 Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
 65 70 75  
 Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr  
 80 85 90  
 Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
 95 100 105

Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115					120
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130					135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145					150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160					165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175					180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
				245					250					255

Ser Arg

<210> 226  
 <211> 3939  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 cggcaaacag cggcggccac caccgctgcc aatggcgccc tgcgggggcc 50  
 atgttgcgtc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100  
 gagccatctg ggggtttctg ggcccaagaa cgtctgcag aaagacgccg 150  
 agtttgagcg caactacgtg gacgaggtca acagcgagct ggtcaacatc 200  
 tacaccttca accatactgt gaccggcaac aggacagagg gcgtgcgtgt 250  
 gtctgtgaac gtctgaaca agcagaaggg ggcgccgttg ctgtttgtgg 300  
 tcggccagaa ggaggtgtg gtgtccttc aggtgcccct aatcctgcga 350  
 gggatgtttc agcgcaagta cctctaccaa aaagtggaa gaacctgtg 400  
 tcagccccc accaagaatg atcggagat tcagttcttc tacgtgatg 450

tgtccacccct gtraccagtc aacaccacat accagctccg ggtcagccgc 500  
atggacgatt ttgtgctcag gactggggag cagttccagct tcaataccac 550  
agracacacag ccacagtaact tcaagtatga gttccctgaa ggctgggact 600  
cggttaattgt caaggtgacc tcbaacaagg ccttccctg ctcagtcato 650  
tcacattcagg atgtgctgtg tccctgtctat gactgggaca acaacgtaga 700  
cttcattggc atgtaccaga cgatgacaa gaaggcggcc atcacctac 750  
agcgcaaaaga cttcccccagc aacagctttt atgtgggggt ggtgggtgaag 800  
accgaagacc aagcctggcg gggctccctg cctttctacc ccttcgcaga 850  
agatgaaccg gtccatcaag ggcacgcaca gaaaacctg tcagtctcgg 900  
tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctcttttgc 950  
ctgggtatat ttctctcctt ttacctgctg accgtccctc tggcctgctg 1000  
ggagaactgg aggcagaaga agaagacctt gctgggtggcc attgaccgag 1050  
cctgcccaga aagcggtcac cctccagctc tggctgattc ttttccctgg 1100  
agttccctct atgaggggta caactatggc tcctttgaga atgtttctgg 1150  
atctaccgat ggtctgggtg acagcctcgg cactggggac ctctcttaac 1200  
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtgga 1250  
tccatgagct ctgtggagga ggtatgactc gacacattga ccgacatga 1300  
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350  
tggcacggaa ggacaagcgt gttctcggga aaaagtacca gatctacttc 1400  
tggaacattg ccaccattgc tgtctctat gcccttccctg tgggtccagct 1450  
ggtgatcacc taccagaagg tggatgaatg cacagggaat caggacatct 1500  
gctaactaaa cttccctctg gccacccac tgggcaatct cagcgccttc 1550  
aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcctttcct 1600  
gctcatcacc ctgcaacggg agatcaacca caacggggcc ctgctgcgca 1650  
atgacctctg tgcctggaa tgtgggatac caaacactt tgggcttttc 1700  
taagccatgg gcacagccct gatgatggag gggctgctca gtgcttgcta 1750  
tcattgtgtc cccaaactata ccaatttcca gtttgacaca tcgttcatgt 1800  
acatgatcgc cggactctgc atgctgaagc tctaccagaa gcggcaccgc 1850  
gaatcaac ccagcgcta cagtgttac gctgtctgg ccattgtcat 1900

tttttttttt gtgtgtggggg tgggttttgg gaaaggggaa aagggttttt 1950  
ggatgtgttt ttccatcatt cacatcatcg ccacccgtgt cctcagcacg 2000  
cagctctatt acatggggcg gtggaaaactg gaactggggga ttttcggcgg 2050  
catctctcac gtgtcttaca cagaactgcat ccggcagtgz agcggggcgg 2100  
tctaagtggg ccgcatgggtg ctgtgtggta tgggcaactg catcaactgg 2150  
tegtgtgtgt cctatgggtt tatcatgccc cccaatgatt tegtctcta 2200  
cttgttggcc attggcatct gcaacctgtt cttttaactt gctttctaca 2250  
tcatcatgaa gctccggagt ggggagagga tcaagctcat cccctgtct 2300  
tgcctgtttt gcaactccgt ggtctggggc ttctgtgttt ttttttttt 2350  
ccagggaact agcaactggc agaaaacccc tgcagagtcg agggagcaca 2400  
acggggaactg catctctctc gaactttttg acgaaccaga catctggcac 2450  
ttctctctct ccctggccat gttcgggttc ttctgggtgt tcttgacact 2500  
ggatgacgac ctggataactg tgcagcggga caagatctat gtcttttagc 2550  
aggagtggg cccttgcctt cactccaagg ggcctgagc tcttttgtgt 2600  
catagacggg tcaactctgt gtgtgtgtgg gatgagtcct agcacggctg 2650  
ccagcaactg gatggcagca ggacagccag gtctagctta ggcttggct 2700  
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gcaggcctgc tccctggaa ccccagatg ttggccaaat tctgtcttct 2800  
ttctcagtgt tggggccttc catgggcccc tgtcttttgg ctctccattt 2850  
gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgct 2900  
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gctctttttt cctcccatc tccactcca gggctagtc tggggcctga 3000  
atctctgtcc tgtatcaggg cccagttct ctttgggtgt tccctggctg 3050  
ccatcaactg ccattccagt cagccaggat ggatgggggt atgagatttt 3100  
gggggttggc cagctgggtg cagaattttg gtgctaaggc ctgcaagggg 3150  
cctggggcag tgcgtattct ctccctctg acctgtgctc agggctggct 3200  
ctttagcaat ggcctcagcc caatttgaga accgccttct gattcaagag 3250  
gctgaattca gaggtcact cttcatccc tcaagctccc gactgatgct 3300

agcaccagga ctggagggag aagggactca ccccttccct tctttctttt 3350  
 caggccctta gtattgcaaa accccagctg gtggcctttt agtgccattg 3400  
 acactgccc aagaatgtcca ggggcaaaag agggatgata cagagttcag 3450  
 cccgttcttg cccacagct gtgggcaccc cagtgcctac cttagaaaag 3500  
 ggcttcagga agggatgtgc tgtttccctc taagtgcaca gtcttagcct 3550  
 agctctagga cccagggctg gctttctaagt ttctgtccag tcttcaggca 3600  
 agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagttttc 3650  
 aaagaattgc cccagctctg ggcacctgg ccacctggt ccttggtacc 3700  
 ccttcgtccc acctggcca cccagatgc tgaggatggg ggagctcagg 3750  
 cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttgttt 3800  
 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850  
 ccagagcgtc tccatgctat ggttgcatth ccgttttcta tgaatgaatt 3900  
 tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 217  
 <211> 832  
 <212> PRT  
 <213> Homo sapiens

<400> 217  
 Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser  
 1 5 10 15  
 Val Gln Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln  
 20 25 30  
 Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser  
 35 40 45  
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn  
 50 55 60  
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln  
 65 70 75  
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val  
 80 85 90  
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg  
 95 100 105  
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro  
 110 115 120  
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser

	125		130		135
Thr Leu Ser Pro	Val Asn Thr Thr Tyr	Gln Leu Arg Val Ser Arg			
	140		145		150
Met Asp Asp Phe	Val Leu Arg Thr Gly	Glu Gln Phe Ser Phe Asn			
	155		160		165
Thr Thr Ala Ala	Gln Pro Gln Tyr Phe	Lys Tyr Glu Phe Pro Glu			
	170		175		180
Gly Val Asp Ser	Val Ile Val Lys Val	Thr Ser Asn Lys Ala Phe			
	185		190		195
Pro Cys Ser Val	Ile Ser Ile Gln Asp	Val Leu Cys Pro Val Tyr			
	200		205		210
Asp Leu Asp Asn	Asn Val Ala Phe Ile	Gly Met Tyr Gln Thr Met			
	215		220		225
Thr Lys Lys Ala	Ala Ile Thr Val Gln	Arg Lys Asp Phe Pro Ser			
	230		235		240
Asn Ser Phe Tyr	Val Val Val Val Val	Lys Thr Glu Asp Gln Ala			
	245		250		255
Cys Gly Gly Ser	Leu Pro Phe Tyr Pro	Phe Ala Glu Asp Glu Pro			
	260		265		270
Val Asp Gln Gly	His Arg Gln Lys Thr	Leu Ser Val Leu Val Ser			
	275		280		285
Gln Ala Val Thr	Ser Glu Ala Tyr Val	Ser Gly Met Leu Phe Cys			
	290		295		300
Leu Gly Ile Phe	Leu Ser Phe Tyr Leu	Leu Thr Val Leu Leu Ala			
	305		310		315
Cys Trp Glu Asn	Trp Arg Gln Lys Lys	Lys Thr Leu Leu Val Ala			
	320		325		330
Ile Asp Arg Ala	Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala			
	335		340		345
Asp Ser Phe Pro	Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly			
	350		355		360
Ser Phe Glu Asn	Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser			
	365		370		375
Ala Gly Thr Gly	Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe			
	380		385		390
Glu Pro Val Gly	Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val			
	395		400		405
Glu Glu Asp Asp	Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys			

410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615
Val Ile Phe Phe Ser Val Leu Gly Val	Val Phe Gly Lys Gly Asn	
620	625	630
Thr Ala Phe Trp Ile Val Phe Ser Ile	Ile His Ile Ile Ala Thr	
635	640	645
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr	Met Gly Arg Trp Lys Leu	
650	655	660
Asp Ser Gly Ile Phe Arg Arg Ile Leu	His Val Leu Tyr Thr Asp	
665	670	675
Cys Ile Arg Gln Cys Ser Gly Pro Leu	Tyr Val Asp Arg Met Val	
680	685	690
Leu Leu Val Met Gly Asn Val Ile Asn	Trp Ser Leu Ala Ala Tyr	

695	700	705
Gly Leu Ile Met Arg Pro Asn Asp Phe	Ala Ser Tyr Leu Leu Ala	
710	715	720
Ile Gly Ile Cys Asn Leu Leu Leu Tyr	Phe Ala Phe Tyr Ile Ile	
725	730	735
Met Lys Leu Arg Ser Gly Glu Arg Ile	Lys Leu Ile Pro Leu Leu	
740	745	750
Cys Ile Val Cys Thr Ser Val Val Trp	Gly Phe Ala Leu Phe Phe	
755	760	765
Phe Phe Gln Gly Leu Ser Thr Trp Gln	Lys Thr Pro Ala Glu Ser	
770	775	780
Arg Glu His Asn Arg Asp Cys Ile Leu	Leu Asp Phe Phe Asp Asp	
785	790	795
His Asp Ile Trp His Phe Leu Ser Ser	Ile Ala Met Phe Gly Ser	
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Phe Leu Val Leu Leu Thr Leu Asp Asp	Asp Leu Asp Thr Val Gln	
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Arg Asp Lys Ile Tyr Val Phe		
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<211> 807

<212> PRT

<213> Homo sapiens

<400> 219

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			20					25				30		

Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
			35					40				45		

Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
			50					55					60	

Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
			65					70					75	

Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
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Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
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His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
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Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
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Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
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Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
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His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
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His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
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Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
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Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
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Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
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Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

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Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala	380		385		390
Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu	395		400		405
Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met	410		415		420
Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val	425		430		435
Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile	440		445		450
Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro	455		460		465
Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu	470		475		480
Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr	485		490		495
Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val	500		505		510
Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser	515		520		525
His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly	530		535		540
Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val	545		550		555
Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu	560		565		570
Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr	575		580		585
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu	590		595		600
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly	605		610		615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp	620		625		630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu	635		640		645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His					

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Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
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Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
800	805	

<110> 230

<111> 50

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 230

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<110> 231

<111> 24

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 231

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<112> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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 <212> PRT  
 <213> Homo sapiens

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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
 35 40 45  
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe  
 50 55 60  
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
 65 70 75  
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
 80 85 90  
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
 95 100 105  
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr  
 110 115 120  
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn  
 125 130 135  
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly  
 140 145 150  
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
 155 160 165  
 Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile  
 170 175 180  
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala  
 185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser	200	205	210
Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro	215	220	225
Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys	230	235	240
Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro	245	250	255
Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp	260	265	270
Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	275	280	285
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn	290	295	300
Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met	305	310	315
Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu	320	325	330
Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val	335	340	345
Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr	350	355	360
Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile	365	370	375
Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly	380	385	390
Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr	395	400	405
Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu	410	415	420

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<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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 <212> PRT  
 <213> Homo sapiens

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 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala  
 200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tttggctgtt ggctatgtg ctcccaacca tgaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactggggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggatatggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

agcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

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ggaccagga atcttgcctt ccagccacaa agagacagat gaagatgcag 250

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25				30	

Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40				45	

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55				60	

Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70				75	

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85				90	

Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100				105	

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
110 115 120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val  
125 130 135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala  
140 145 150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala  
155 160 165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala  
170 175 180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
185 190 195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
200 205 210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala  
215 220 225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
230 235 240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala  
245 250 255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
260 265 270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala  
275 280 285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
290 295 300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala  
305 310 315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala  
320 325 330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val  
335 340 345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala  
350 355 360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala  
365 370 375

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala  
380 385 390

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				395					400					405
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				410					415					420
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Glu	Ala	Ser	Thr	Ala
				425					430					435
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val
				440					445					450
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala
				455					460					465
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ala	Gly	Ser	Gly	Thr	Ala
				470					475					480
Ala	Leu	Thr	Gly	Met	His	Thr	Thr	Ser	His	Ser	Ala	Ser	Thr	Ala
				485					490					495
Val	Ser	Glu	Ala	Lys	Pro	Gly	Gly	Ser	Leu	Val	Pro	Trp	Glu	Ile
				500					505					510
Phe	Leu	Ile	Thr	Leu	Val	Ser	Val	Val	Ala	Ala	Val	Gly	Leu	Phe
				515					520					525
Ala	Gly	Leu	Phe	Phe	Cys	Val	Arg	Asn	Ser	Leu	Ser	Leu	Arg	Asn
				530					535					540
Thr	Phe	Asn	Thr	Ala	Val	Tyr	His	Pro	His	Gly	Leu	Asn	His	Gly
				545					550					555
Leu	Gly	Pro	Gly	Pro	Gly	Gly	Asn	His	Gly	Ala	Pro	His	Arg	Pro
				560					565					570
Arg	Trp	Ser	Pro	Asn	Trp	Phe	Trp	Arg	Arg	Pro	Val	Ser	Ser	Ile
				575					580					585
Ala	Met	Glu	Met	Ser	Gly	Arg	Asn	Ser	Gly	Pro				
				590					595					

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggtgtgga taga 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggaccagagc atottgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gogtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cactgtctggc cggctcctgc 100

tcctctccttc tgcactggg ggccctgtct ggatggggcg ccagcgatga 150

cccatatgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagajaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcac 250

ggcggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccatcccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

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caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650

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<210> 248  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 248  
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 20 25 30  
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg  
 35 40 45  
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His  
 50 55 60  
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met  
 65 70 75  
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu  
 80 85 90  
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile  
 95 100 105  
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn  
 110 115 120  
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln  
 125 130 135  
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys  
 140 145 150  
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu  
 155 160 165  
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala  
 170 175 180  
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 250  
 aagttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 251  
 tgaacccatt gagaaggcca ttgaagggat caaccgaggg ctg 43

<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile	125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly	140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn	155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp	170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala	185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe	200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro	215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe	230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly	245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu	260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile	275	280	285
Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp	290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp	305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro	320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr	335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val	350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys	365	370	375
Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405

Gln Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
				695					700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
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Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
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Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
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Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
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Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
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<210> 258

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<212> DNA

<213> Homo sapiens

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<223> unknown base

<400> 259

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<211> 802

<212> FRT

<213> Homo sapiens

<400> 260

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Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
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Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
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Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
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Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
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Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
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Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
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Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	

	275		280		285
Lys Gly Tyr Ile Arg Asp Leu His Asn Ser	290	Lys Ile His Gln Ala	300		
Ile Thr Leu His Pro Asn Lys Asn Pro	305	Pro Tyr Gln Tyr Arg Leu	315		
His Ser Tyr Met Leu Ser Arg Lys Ile Ser	320	Glu Leu Arg His Arg	330		
Thr Ile Gln Leu His Arg Glu Ile Val Leu	335	Met Ser Lys Tyr Ser	345		
Asn Thr Glu Ile His Lys Glu Asp Leu Gln	350	Leu Gly Ile Pro Pro	360		
Ser Phe Met Arg Phe Gln Pro Arg Gln Arg	365	Glu Glu Ile Leu Glu	375		
Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr	380	Ser Ala Val Asp Gly	390		
Gln Pro Pro Arg Arg Gly Met Asp Ser Ala	395	Gln Arg Glu Ala Leu	405		
Asp Asp Ile Val Met Gln Val Met Glu Met	410	Ile Asn Ala Asn Ala	420		
Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys	425	Glu Ile Gln Tyr Gly	435		
Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala	440	Glu Tyr Ile Leu Asp	450		
Leu Leu Leu Leu Tyr Lys Lys His Lys Gly	455	Lys Lys Met Thr Val	465		
Pro Val Arg Arg His Ala Tyr Leu Gln Gln	470	Thr Phe Ser Lys Ile	480		
Gln Phe Val Glu His Glu Glu Leu Asp Ala	485	Gln Glu Leu Ala Lys	495		
Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser	500	Phe Leu Ser Asn Ser	510		
Leu Lys Lys Leu Val Pro Phe Gln Leu Pro	515	Gly Ser Lys Ser Glu	525		
His Lys Glu Pro Lys Asp Lys Lys Ile Asn	530	Ile Leu Ile Pro Leu	540		
Ser Gly Arg Phe Asp Met Phe Val Arg Phe	545	Met Gly Asn Phe Glu	555		
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val		Lys Leu Val Val Leu			

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Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
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Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
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Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
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Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
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Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 262

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

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<400> 263

ccagaagaag tcttccatga tgcacaagta catgcacgac cactac 46

<210> 264

<211> 1419

<212> DNA

<213> Homo sapiens

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 aaaaatttta aacctacttg atattccata acaaagctga ttttagcaaa 1250  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60

Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75

Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
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Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly		
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Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro		
				110					115					120		
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala		
				125					130					135		
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu		
				140					145					150		
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val		
				155					160					165		
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro		
				170					175					180		
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu		
				185					190					195		
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys		
				200					205					210		
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp		
				215					220					225		
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala		
				230					235					240		
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu		
				245					250					255		
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala		
				260					265					270		
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro		
				275					280					285		
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile		
				290					295					300		
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp		
				305					310					315		
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val		
				320					325					330		
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala		
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Leu	Leu	Lys	Val	Tyr												
				350												

<210> 266

<211> 2403

<212> DNA

>213> Homo sapiens

>471> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20				25					30	

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
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35										40					45				
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
				140					145					150					
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
				155					160					165					
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
				215					220					225					
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val					

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Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val					
	335		340		345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp					
	350		355		360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn					
	365		370		375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr					
	380		385		390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr					
	395		400		405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe					
	410		415		420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys					
	425		430		435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr					
	440		445		450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp					
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<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 gtcattctca tatccctgat tgccttggca gtgtgcattg gactcactgt 150  
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 aacaatttta cagaaatgag ccagagacctt gaatcaatgg tgaaaaatgc 300  
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 agttcagtc aacagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
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 tgttttacat gaaaagctgc aagatgttgt agtaacctct aaagtagatc 500

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 atgataaatg tgaagaagat tctgtttttt tgtgaactat aataattata 2000  
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 <211> 423  
 <212> PFT  
 <213> Hcmo sapiens

<400> 269  
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 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210

Trp Asp Gly Ser	His Arg Cys Gly Ala Thr	Leu Ile Asn Ala Thr
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Trp Leu Val Ser	Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro	
230	235	240
Ala Arg Trp Thr	Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys	
245	250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys	
260	265	270
His Pro Ser His	Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser	
275	280	285
Pro Val Pro Tyr	Thr Asn Ala Val His Arg Val Cys Leu Pro Asp	
290	295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly	
305	310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg	
320	325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro	
335	340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly	
350	355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly	
365	370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly	
380	385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly	
395	400	405
Val Tyr Thr Arg	Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys	
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<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
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<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe  
 50 55 60  
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile  
 65 70 75  
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu  
 80 85 90  
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 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met  
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				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser
				170					175					180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln
				185					190					195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met
				200					205					210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe
				215					220					225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu
				230					235					240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro
				245					250					255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His
				260					265					270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg
				275					280					285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe
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				305										

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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 35 40 45  
 Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr  
 50 55 60  
 Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln  
 65 70 75  
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 80 85 90  
 His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg  
 95 100 105  
 Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr  
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 140 145 150  
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn  
 155 160 165  
 Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser  
 170 175 180

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	185	190	195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	200	205	210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	215	220	225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	230	235	240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	245	250	255
Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	275	280	285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	290	295	300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	305	310	315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	320	325	330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	365	370	375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
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<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<211> 761

<212> PFT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

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Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser	Thr
230	235	240	
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe	Asp
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Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr	Thr
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Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu	Pro
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Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln	Val
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Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu	Asp
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Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu
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Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg
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Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr
380	385	390	
Phe Met Lys Asp	His Phe Leu Met Asp	Gln Gln Val Val Gly	Thr
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Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr
425	430	435	
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly
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Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp
455	460	465	
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala
470	475	480	

Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala	755	760	

<210> 278  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 278  
cttcttggtga aatctggcgt ggag 24

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
catcttgatca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
agggtccctt agccgggcgc agggcgcgca gccaggctg agatccgcgg 50  
cttcggtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100  
ttcttctcc ctggggtcct gctctcagag gctgccaaaa tctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacggtcat aatgtacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatacatg gattocttaa agaattagaa ottogacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550  
tttgtggcca ttctttccac ttcattoggo tctttggaat ttgggtaccc 600  
aatcccttg tcttatgttc cagtattccg ttcttgctg actgatcaca 650  
tggaactctg gggccagatg aagaatttct tgatgttctt tagttctctg 700  
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
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agttgtgggt cattaactct gaactttgct ttgattttgc tcgacctctg 850  
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900  
agtaaccaca gaacttgaga acttcattgc caagtttggg gactctggtt 950  
ttgtccttgt gaacttgggc tccatggtga acactgtca gaatccggaa 1000  
atcttcaagg agatgaacaa tgcctttgct cactacccc aaggggtgat 1050  
atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
atgtgaaaat tgtggaactg ctctctcaga gtgaactcct ggcacacca 1150  
agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggo 1200  
caccagcat ggtgtgcca tggtggggat cctctctctt ggagaccagc 1250  
ctgaaaacat ggtccagatg gaagccaaaa agtttggtgt ttctattcag 1300  
ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350  
ggaagacaag agatacaagt ccggggcagt ggtgcccagt gtcactctg 1400  
gtcccaccc gtcagcccc acacagggg tggtgggctg gattgaccac 1450  
gtctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500  
gpcctggcat gagcagtacc tgttcagct ttttgtgtt ctgtggggg 1550  
tcactctggg gactctatgg ctctgtggga agctgtggg catggctgtc 1600  
tggtggtgc gtggggccag aaaggtgaag gagacataag gccaggtgca 1650  
gccttgggg ggtctgtttg gtgggggatg taccatttc tagggagctt 1700  
ccactagtt ctggcagccc cattctctag tcttctagt tatctctgt 1750  
tttcttgaag aacaggaaaa atggccaaaa atcatcctt ccacttgcta 1800  
atcttgctac aaattcctc ttaactagct ctgctgcta gcagaaatct 1850

ttccagtcct cttgttcctc tttgtttgca atcagcaagg gctatgctgt 1900  
 gattctgtct ctgagtgaact tggaccactg acctcagat ttccagcctt 1950  
 aaaatccacc ttctttctca tggcctcttc cgaatcacac cctgactctt 2000  
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcctctact 2050  
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100  
 ttctgttttg ttctccaca tattctcttc aatgttcagg aagcctgcc 2150  
 tgtgcttgag agttcagggc cggacacagg ctccacaggtc tccacattgg 2200  
 gtccctgtct ctggtgccca cagtgaagtc cttcttggct gagcaggcat 2250  
 ggagaactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgtta 2300  
 tctctcccca acctcactaa 2320

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282  
 Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro  
 1 5 10 15  
 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr  
 20 25 30  
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile  
 35 40 45  
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg  
 50 55 60  
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln  
 65 70 75  
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys  
 80 85 90  
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly  
 95 100 105  
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln  
 110 115 120  
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys  
 125 130 135  
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys  
 140 145 150  
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu	Phe Gly Leu Pro Ile Pro	
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser	Leu Leu Thr Asp His Met	
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe	Leu Met Phe Phe Ser Phe	
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser	Thr Phe Asp Asn Thr Ile	
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg	Pro Val Leu Ser His Leu	
230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile	Asn Ser Asp Phe Ala Phe	
245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn	Thr Val Tyr Val Gly Gly	
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr				
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp				
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu				
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala				
	500		505		510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr					
	515		520		

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 283  
 tgcctttgct cacctacccc aagg 24

<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 284  
 tcaggctggg ctocaaagag aggg 24

<210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 285  
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaag; 50

ggttgagggg ctgctcttgg catatgcaca caactacaca ttctgtcaca 110  
cccgtcacac acacatacca tgtttctccat ccccccaggt ccagcctcca 150  
gtgctgtccc atccagcagg gctaccctga agctctgggt gcagcctccc 200  
cgctccagtgg gcaggcggtt tcatccctcc tttctctccc aaagcccaac 250  
tgetgtcact gcctgtcttg ccaaggagga gggaaactga gtgacagpag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400  
ccaggggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450  
gggttgacga gccctccagc catgttggga gccaaagcac actggctacc 500  
aggtcccta cacagtcctg ggctgcctt gggtctgggt cttctggccc 550  
tgggggccgg gtgggcccag gaggggtcag agcccgctct gctggagggg 600  
gagtgcctgg tggctctgtg gcctggccga gctgttcag gggggcccgg 650  
gggagcagcc ctgggagagg caccccctgg gcgagtggca tttgctgcgg 700  
tcogaagcca ccaccatgag ccagcagggg aaacccggca tggcaccagt 750  
ggggccatct acttcgacca ggctctgggt aacgagggcg gtggcttga 800  
ccgggcctct ggctccttcg tagccctgt ccgggggtgt tacagcttcc 850  
ggttccatgt ggtgaagggt tacaacccgc aaactgtcca ggtgagcctg 900  
atgctgaaca ctgggcctgt catctcagcc tttgcacatg atcctgacgt 950  
gaccggggag gcagccacca gctctgtgt actgccttg gaccctgggg 1000  
aacgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
tactcaagtt tctctggctt cctcatcttc cctctctgag gaccaagtc 1100  
tttcaagcac aagaatccag cccctgacaa cttctctctg cctctcttg 1150  
ccccagaaac agcagaggca ggagagagac tccctctggc tctatccca 1200  
cctcttttga tgggaacctg tgccaaacac ccaagtttaa gagaagagta 1250  
gagctgtggc atctccagac caggcctttc caccaccca cccccagtta 1300  
ccctccagc cactgtctgc atctgttctt gctgcagcc ctaggatcag 1350  
ggcaaggttt ggcaagaagg aagatctga ctactttggg gcctctgtc 1400  
ctccggttcc cccaccccag cttcctgtc aatgtgtac agggacaggt 1450

ggagcagggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcagggato 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600  
 aggcctcagcc acaggcagaa ggggtgggaag ggccctggagt ctgtggcttg 1650  
 tgaggaagga aggaggggtgt attgtctaga ctgaacatgg tacacattct 1700  
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
 gctggatccc agatggactc tggcccttac ctcccccact gagattaggg 1800  
 tgagtgtgtt tgcctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccattgcctc tcttgcttgg 1900  
 ccacctctctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 caactctgact gctgcctcct tctcccagc tctctcactg agttatcttc 2000  
 actgtacctg ttccagcata tcccactat ctctcttctc cctgatctgt 2050  
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 ccttcttcca gacctctcc tgcagtatg ctaaaacctc cctctctctt 2150  
 tcttatcccg ctgtccatt ggcccagcct ggtatgaatct atcaataaaa 2200  
 caactagaga atggt-ggtca gt-gagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser  
 1 5 10 15

Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly  
 20 25 30

Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys  
 35 40 45

Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly  
 50 55 60

Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala  
 65 70 75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 238

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

agggcagggcac cagctctgtg ctac 24

<210> 299

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 269

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<4300> 290

ctgtgtactt gctcttggac cctgggggacc gactgtctct gc 42

<4210> 291

<4211> 1670

<4212> DNA

<4213> Homo sapiens

<4400> 291

gctgtttctc tctgctccac actggccgcc ggcgcagct ccaggtgtcc 50

tagccgccca gctctgacgc cgtcccgga cccctgtgt ctgcgcgaag 100

ccctggccccc gggggccggg gcatgggcca ggggcgggg gtgaagcggc 150

ttcccggggg gccgtgactg ggccggcttc agccatgaag accctcatag 200

ccgctactc cggggctctg ccggcgagac gtcaggccga ggcagacgg 250

agccagcgt ctccaggag acctgccgt tgcgcgagg ggtctgggag 300

atggggcact ggatccagca tctctccgc cctccaggac ctctctctg 350

tcacctgggt caataggctc aagggtgaaa agcagctaca ggtcatctca 400

gtgctccagt gggctctgtc ctctctgtg ctgggagtg cctgcagtgc 450

cactctcatg tacatattct gcactgatt ctggctcctc gctgtgtct 500

acttcacttg gctggtgttt gactggaaca caccacaaga aggtggcagg 550

aggtcacagt gggctccgaaa ctgggctgtg tggcgctact ttgagacta 600

ctttcccatc cagctggtga agacacaca cctgtcgacc accaggaact 650

atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700

aacttcagca cagaggccac agaagtgagc aagaagtcc caggcatacg 750

gccttacctg gctacactgg caggcaactt ccgaatgct gtgttgaggg 800

agtaactgat gtctggaggt atctgcctg tcaggcggga caccatagac 850

tatttgcttt caaagaatgg gactggcaat gctatcatca tctggtctcg 900

gggtgoggct gactctctga gctccatgcc tggcaagaat gcagtcaccc 950

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cacacctggg ggtggtgccc ctactccaag cccatccca ctgttggtgg 1200

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 cacaagacca agttgggctt cccggagaat gaggtcctgg aggtgaactg 1350  
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400  
 tttgtctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttaaaa 1450  
 gaaattataa caattttgt aaacccaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292  
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu  
 1 5 10 15  
 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro  
 20 25 30  
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser  
 35 40 45  
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn  
 50 55 60  
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln  
 65 70 75  
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile  
 80 85 90  
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu  
 95 100 105  
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly  
 110 115 120  
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr  
 125 130 135  
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu  
 140 145 150  
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile  
 155 160 165  
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu  
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	380	385	

<210> 193

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

jctgacgtgg ttcccatcta ctcc 24

<210> 194

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggggggggg atgggggggg gggggggggg ggggggcaact cgctgaggcc 50

ccgacgcagg gcgggggggg gcccagggcc gaggagcgcg gcggccagag 100

cgggggcgcg gaggcgagcg cgggggagcc cggcgagcga gcaggtggcg 150

ggggctgcag gcttgctcag ccggaagccc tgagggcagc tgttccact 200

ggctctgctg accttgctgc ttggacggct gtctcagcg agggggcctg 250

caccgcctcc tgagcagcgc catgggctg ctggccttcc tgaagacca 300

gttcgtgctg caactgctgg tcggctttgt cttcgtggcg agtggctctg 350

tcataaactt cgtccagctg tgcaagctgg cgtctggccc ggtcagcaag 400

cagctctacc gcggctcaa ctgcggctc gctactcac tctggagcca 450

actggtcatg ctgctggagt ggtggctctg caggagtggt acactgttca 500

cggaccaggc cagggtagag cgttttgga aggagcagc agtcacatc 550

ctcaaccaca acttcagat cgaattctc tgtgggtgga ccattgtgtg 600

gggcttcgga gtgctggga gctccaaagt cctcgctaag aaggagctgc 650

tctacgtgac cctcatcggc tggacgtggt actttctgga gattgtgttc 700

tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtgag 750

ggcgctgtcg gactacccg agtacatgtg gtttctctg tactgagagg 800

ggaagagatt caaggagacc aagcaccggg tttagcatgga ggtggagggt 850  
gctaaggggg ttctgtctct caagtaccac ctcttgaggg ggaaccaagg 900  
cttcaccacc gcagtcaggt gctccggggg gacagtcgca gctgtctatg 950  
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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
			20					25					30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
			35					40					45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
			50					55					60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
			65					70					75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 298  
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<210> 299  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 299  
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<210> 300  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 300  
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<210> 301  
 <211> 1334  
 <212> DNA  
 <213> Homo sapiens

<400> 301  
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 tgccttagca ctgggggcact tcttgcttat ttctttggta ggaaaggggc 150  
 tcagtttgtc ttgtgggggtt ggtggcaggc aggcgcggtt acgcctgata 200  
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 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
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gtatggcccc tgccccccctg gccagattca ttgtacatgt ggtgtttctct 450  
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 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
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 ttcctttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
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 cgttgactgt gcttgtgaat tatctgggga tgcaggtctt gattcagtag 950  
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 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25					30	

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40					45	

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55					60	

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	65	70	75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr			
	80	85	90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln			
	95	100	105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu			
	110	115	120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr			
	125	130	135
Cys Gly Val Leu Leu Ser Phe Leu			
	140		

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 tatgtctgtg tggctagtgc tctactcct acctacatta aaatctgttt 200  
 tttgtttctt tgtaactaga ctttaacctt ctaacacaga ggatctgtca 250  
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 ggcgatggct cccactgcac aggcctcaga cttgtctgtg tcaatcactg 550  
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 aattatgggt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
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 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305  
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 ccggctctcc gtgcgcgcgc cgtctggccct gggctcagcc gcaactgggcg 150  
 ccgccttcgc cactggcctc ttccctgggga ggcgggtgcc cccatggcga 200  
 ggcggggag agcagtgcct gctcccccgc gaggacagcc gcctgtggca 250  
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 ccggcggaag tcagggtcta cctcagcctc ctgcctctgg gcgatggact 850  
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 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala	1	5	10	15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe	20	25	30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys	35	40	45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser	50	55	60	
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75	
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90	
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105	
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120	
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135	
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150	
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165	
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180	
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195	
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210	
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225	
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240	
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255	

Leu Thr Leu Ala Phe Lys Ile  
260

<210> 307  
<211> 2272  
<212> DNA  
<213> Homo sapiens

<400> 307  
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gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150  
ggatgggcgc gtgaagcccc caccacaaca gtaccccatc tttttcttgc 200  
gcacacacga aacagccttc ctgggaacca aggaacctgt cccctacgac 250  
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ggcagtgcgc ctgacgagga ccatgaggac cgggggggtc tggcgtcac 450  
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<212> PRT

<213> Homo sapiens

<400> 308

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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

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Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro					
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Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys					
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Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala					
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Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala					
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Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp					
				110					115					120					
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala					
				125					130					135					
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser					
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Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
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Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
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Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
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Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
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Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
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Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
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Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
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Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
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Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
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Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
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Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
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Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg			
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425										430				435			
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg			
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Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser			
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Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro		
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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75

Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105

Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120

Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225

His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
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Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Arg Glu Ser Ser Gln Glu			
	260	265		270	
Gly Ser Thr Ser	Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg Val			
	275	280		285	
Cys Lys Asn Asp	Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys Trp			
	290	295		300	
Thr Thr Phe Leu	Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly Ser			
	305	310		315	
Asp Gly Ala Asp	Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr Leu			
	320	325		330	
Leu Pro Thr Arg	Asp Glu Arg Asn Pro	Val Val Tyr Gly Val Phe			
	335	340		345	
Thr Thr Thr Ser	Ser Ile Phe Lys Gly	Ser Ala Val Cys Val Tyr			
	350	355		360	
Ser Met Ala Asp	Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala His			
	365	370		375	
Lys Glu Ser Ala	Asp His Arg Trp Val	Gln Tyr Asp Gly Arg Ile			
	380	385		390	
Pro Tyr Pro Arg	Pro Gly Thr Cys Pro	Ser Lys Thr Tyr Asp Pro			
	395	400		405	
Leu Ile Lys Ser	Thr Arg Asp Phe Pro	Asp Asp Val Ile Ser Phe			
	410	415		420	
Ile Lys Arg His	Ser Val Met Tyr Lys	Ser Val Tyr Pro Val Ala			
	425	430		435	
Gly Gly Pro Thr	Phe Lys Arg Ile Asn	Val Asp Tyr Arg Leu Thr			
	440	445		450	
Gln Ile Val Val	Asp His Val Ile Ala	Glu Asp Gly Gln Tyr Asp			
	455	460		465	
Val Met Phe Leu	Gly Thr Asp Ile Gly	Thr Val Leu Lys Val Val			
	470	475		480	
Ser Ile Ser Lys	Glu Lys Trp Asn Met	Glu Glu Val Val Leu Glu			
	485	490		495	
Glu Leu Gln Ile	Phe Lys His Ser Ser	Ile Ile Leu Asn Met Glu			
	500	505		510	
Leu Ser Leu Lys	Gln Gln Gln Leu Tyr	Ile Gly Ser Arg Asp Gly			

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Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala
				530					535					540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp
				545					550					555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala
				560					565					570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp
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Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val
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Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro
				605					610					615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly
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Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys
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Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser
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Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
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Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
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Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
				695					700					705
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
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Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
				725					730					735
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
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Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
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<211> 45

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

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(210) 315  
 (211) 370  
 (212) PRT  
 (213) Homo sapiens

(400) 315  
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 35 40 45  
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg  
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 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu  
 65 70 75  
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala  
 80 85 90  
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser  
 95 100 105  
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp  
 110 115 120  
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu  
 125 130 135  
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro  
 140 145 150

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	305	310	315
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	320	325	330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	335	340	345
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	350	355	360
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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				20					25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
				35					40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
				50					55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
				65					70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
				80					85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
				95					100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
				110					115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
				125					130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
				140					145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
				155					160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
				170					175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
				185					190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
				200					205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
				215					220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
				230					235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
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Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala		
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn		
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
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Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro		
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val		

530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly		
545	551	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn		
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Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu		
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Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe		
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Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro		
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Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr		
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Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser		
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Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala		
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Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys		
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Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly		
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Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile		
695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro		
710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser		
725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
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<211> 23

<212> DNA

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<213> Synthetic oligonucleotide probe

<400> 318

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<212> DNA

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<213> Synthetic oligonucleotide probe

<400> 320

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<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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 acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
 tcactctgctg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
 gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
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<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80	85	90
Arg Ser Gly Asn Gly Thr Asp Glu Thr	Leu Glu Val His Asp Phe	
95	100	105
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe	Val Gly Leu Gln Lys Cys	
110	115	120
Phe Ile Lys Thr Gln Ile Lys Val Ile	Pro Glu Phe Ser Glu Pro	
125	130	135
Glu Glu Glu Ile Asp Glu Asn Glu Glu	Ile Thr Thr Thr Phe Phe	
140	145	150
Glu Gln Ser Val Ile Trp Val Pro Ala	Glu Lys Pro Ile Glu Asn	
155	160	165
Arg Asp Phe Leu Lys Asn Ser Lys Ile	Leu Glu Ile Cys Asp Asn	
170	175	180
Val Thr Met Tyr Trp Ile Asn Pro Thr	Leu Ile Ser Val Ser Glu	
185	190	195
Leu Gln Asp Phe Glu Glu Glu Gly Glu	Asp Leu His Phe Pro Ala	
200	205	210
Asn Glu Lys Lys Gly Ile Glu Gln Asn	Glu Gln Trp Val Val Pro	
215	220	225
Gln Val Lys Val Glu Lys Thr Arg His	Ala Arg Gln Ala Ser Glu	
230	235	240
Glu Glu Leu Pro Ile Asn Asp Tyr Thr	Glu Asn Gly Ile Glu Phe	
245	250	255
Asp Pro Met Leu Asp Glu Arg Gly Tyr	Cys Cys Ile Tyr Cys Arg	
260	265	270
Arg Gly Asn Arg Tyr Cys Arg Arg Val	Cys Glu Pro Leu Leu Gly	
275	280	285
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln	Gly Gly Arg Val Ile Cys	
290	295	300
Arg Val Ile Met Pro Cys Asn Trp Trp	Val Ala Arg Met Leu Gly	
305	310	315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 ggccgtgcag cttctgggtt tctgtctag cttctgggc atggtgggca 150  
 cgttgatcac caccatcctg ccgcactggc ggaggacaga gcacgtgggc 200  
 accaacatcc tcacggcctg gtctacctg aaagggctct ggatggagt 250  
 tgtgtggcac agcacaggca tctaccagt ccagatctac ccatcctgc 300  
 tggcgtgcc ccaagacctc caggctgccc gcgcctcat ggtcatctcc 350  
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 cacgcgtgc gccaaaggga caccgcaca gaccacctt gccatcctc 450  
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 ataccaaaaga ctgaaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttgga 1100  
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 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20		25		30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35		40		45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50		55		60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65		70		75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80		85		90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95		100		105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110		115		120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125		130		135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140		145		150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155		160		165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170		175		180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185		190		195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200		205		210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215		220		225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230		235		

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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gcacggggc caccgggatg gacatytga gcaccaggga cctgtaagac 200

aaccccgtaa cctccgtgtt ccagtaacgaa gggctctgga ggagctgggt 250  
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gtgtttgcca acatgctggg gactaaactc tggatgtcca cagctaacat 550  
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ttgggtgcggc tctgttcgtg ggtcgggtcg ctggaggcct cactactaatt 650  
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cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
cccatgatct cggttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
tcttattaca gcaacaccat tctaggagtt tctgagctc tccactggag 1550  
tctctttctt gtgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600

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 taaaatgata cactatctct gtgaaatagc ctacacctta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcactttgg gaggetgagg aggaaggatc acttgagccc agaagttoga 1850  
 gactagcctg ggcaacatgg agaagcctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggetgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245					250					255
Ser	Lys	His	Asp	Tyr	Val									
				260										

\*210\* 327  
 \*211\* 2010  
 \*212\* DNA  
 \*213\* Homo sapiens

\*400\* 327  
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 caaccccatgc cttagaaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
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 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350  
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 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450  
 ctgtgacgg ctggaatcat ctccatcac acgggcatgg tgggtgctcat 500  
 cctgtgagc tgggttgcca atgcatcat cagagatttc tataactcaa 550  
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 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgtgctg 650

tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaaac ccaaaaaaagt tatcacacccg gaaagaaagtc aaccgagcgtc 750  
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 caaagaaaact ttgatttact gttcttaact gcttaacttt aattacagga 900  
 actgtgcato agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgtttctaga aagtatagta atttgttttc 1000  
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 tgcataagac tgcattatct tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctccataga gacatgctta 1150  
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 actcaactat tgccttttcag ggaaatcatg gatagggttg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcttc catttataat 1300  
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 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
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 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
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<211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	215	220	225	

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 329

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 gcctgtggat gtctcgtg gtgcagagca ccggccagat gcagtgcag 200  
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 cgcctgggtc tcacctctgg gattgtcttt gtcctctcag gggctcctgc 400  
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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu	
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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp	
				20					25					30	
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val	
				35					40					45	
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	
				50					55					60	
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val	
				80					85					90	
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr	
				95					100					105	
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr	
				110					115					120	
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro	
				125					130					135	
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	
				140					145					150	
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr	
				155					160					165	
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Gly	Gly	Gly	Gly	Leu	
				170					175					180	
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His	
				185					190					195	
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly	
				200					205					210	
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val						
				215					220						

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50

tttatcatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100

gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tgggtcttgg 150  
 gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggt 200  
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
 ggaagggctc tggatgaatt gcctccgaca agccagggtc cggttgcaat 300  
 gcaagttcta tagctccttg ttggtctctc cgcctgcctt ggaaacagcc 350  
 cgggcctca tgtgtgtggc tgttgctctc tcttgatcg cctgtcttat 400  
 tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450  
 ccaaagcata ccttctggga acttcaggag tctcttctcat cctgaagggt 500  
 atcttcgttc tgattccggg gagctggaca gccaatataa tcctcagaga 550  
 tttctacaac ccagccctcc acatagggtc gaaacgagag ctgggagcag 600  
 cacttttctc tggctgggca agcgtgctg tctcttctcat tggagggggg 650  
 ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700  
 tccagtgcct ggctaccgtg tgcacacac agataagcga agaaatacga 750  
 caatgcttag taagacctcc accagttatg tctaattgct ccttttggct 800  
 ccaagtatgg actatggta atgtttttta taaagtctg ctagaaactg 850  
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
 cgaaagtctc aatttgctac tgggtgtagg aatgaaaatg acttacttgg 950  
 acattctgac ttcaggtgta ttaaattgat tgactattgt tggaccaat 1000  
 cgtgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
 caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100  
 ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150  
 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

	35		40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn					
	50		55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe					
	65		70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala					
	80		85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly					
	95		100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser					
	110		115		120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys					
	125		130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly					
	140		145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu					
	155		160		165
Ser Lys Thr Ser Thr Ser Tyr Val					
	170				

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50  
 atcaactgggg gtctccttct gctctgtaca gtgggtctatt tctgtagcag 100  
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggc atccctgccc ccattacata cctaccagtt 200  
 tgtgggtctg actacatcac ctatgggaat gaatgtcact tgtgtaccca 250  
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaaagt 450  
 ttctgtgcta cccctacaaa cccatgcttc actgacagac cagcattttt 500  
 ttcttaacac gtcaataaaa aaataattct ccaga 535

<210> 334  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 334  
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
     1                    5                    10                    15  
 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
                     20                    25                    30  
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
                     35                    40                    45  
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
                     50                    55                    60  
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
                     65                    70                    75  
 Arg Val Gln Phe Leu His Asp Gly Ser Cys  
                     80                    85

<210> 335  
 <211> 742  
 <212> DNA  
 <213> Homo sapiens

<400> 335  
 cccgcgcgcg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50  
 ctgctcgccc cccgcgcgca tggctgcctc cccgcgcggg cctgctgtcc 100  
 tggccctgac cgggctggcg ctgctcctgc tctgtgtgtg gggcccaggt 150  
 ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200  
 tgttccaaact aagaactaaag tggccgttga tgagaataaa gccaaagaat 250  
 tctttggcag cctgaagcgc cagaagcggc agctgtggga cgggactcgg 300  
 cccgaggtgc agcagtggtg ccagcagttt ctctacatgg gctttgatga 350  
 agcgaaattt gaagatgaca tcaactattg gcttaacaga gatcgaaatg 400  
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
 gcaattggtc cccggagccc ctacggcttt aggcattggg ccagcgtcaa 500  
 ctacgatgac tactaaccat gacttgcac acgctgtaca agaagcaaat 550  
 agcgattctc ttcattgata tctaatgcc ttacactact tggtttctga 600  
 tttgtcttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
 gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700

ctctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
1 5 10 15  
Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
20 25 30  
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
cggtctcgagc ccgccccgaa gtgcccagagg ggcccgcgatg gagctggggg 50  
agcggggggc tcggtagcgc ggccgggcaag gcaggcgcca tgacctgat 100  
tgaaggggtg ggtgatgagg tgacctctct tttctcgggtg cttgcctgac 150  
ttctgggtgt ggcccttgcc tgggtctcaa cgcaaccgc tgagggcggg 200  
gacctactgc ccagccgtc agggacccca accgatccc agcccagcgc 250  
agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

ccccagcct gagacacaga ggtcaagctg cacagccaga gccagccag 350  
gggttcacag caacacccgc agcccgggac tccccgcagg agcccctcgt 400  
gctacggctg aaatttcctc atgattcaga gcaggtgggc agggcctggc 450  
cccacgacac cattggctcc ttgaaaagga ccagtttcc cggccgggaa 500  
cagcagggtg gactcatctc ccaagggcag ctgctaggcg acgacacca 550  
gacctggggc agccttcacc tccctcccaa ctgctttctc cactgcccag 600  
tgtccacgag agtcggctcc ccaaatcccc cctgcccgcg ggggtccgag 650  
cccggcccc cggggctgga aatcggcagc ctgctgctgc cctgctgt 700  
cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
ttccctgac ccgaactctg ggctggcg gcttcacct gctctcagt 800  
ctcctggcct ttgcctgta ccgcccgtag tgcctccgcg ggcgcttggc 850  
agcgtccgcg gccctccgg accttgctcc ccgcgcgcg gggggagctg 900  
ctgcctgccc aggcccgcct ctcggcctg cctcttcccg ctgcctgga 950  
gcccagccct gcgcgcaga ggaactccgg gactggcgga ggcccgcgcc 1000  
tgcgacccgc ggggtccgg gccacctccc ggggtgctg aacctcagcc 1050  
cgaactggga gtgggtcct ccgggtccgg catctgctgt cgtgcctcg 1100  
gcccggggca gaggccgggc gccccgggg ccggtcttag tgttctgccc 1150  
gaggacccag ccgcctccaa tccctgacag ctcttgggc tgagttgggg 1200  
acgcacggtc ggtgggaggg tgggaaggg gagggggag gggcagagga 1250  
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaa 1300  
aaaaaaaaa 1310

<L10> 338  
<L11> 246  
<L12> PRT  
<L13> Homo sapiens

<I00> 338  
Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe  
1 5 10 15  
Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
20 25 30  
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagcaggt tggagcagtg agtgagtaag gaaacctggc 50

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caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150

atgacaaagg cgtactcat ctatttggtc agcagcttcc ttgcctctaa 200

traggccagc ctcatcagtc gatgtgaatt ggcacaggtg ctgacgtgg 250

aggaacttggga tgggttttgag gggttaactccc tgagtgaactg gctgttgcccg 300  
 gctttttgtgg aaagcaagtt caacatatca aagataaatg aaaaatggcgga 350  
 tgggaagcttt gactatggcc tottccagat caacagccac tactgggtgca 400  
 acgattataa gaggtaactcg gaaaaccttt ggcacgtaga ctgtcaagat 450  
 ctgttgaata ccaacctttct tgcagggcct cactggcgaa aaaggattgt 500  
 gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550  
 caggccggcc actctctctac tgggtgacag gatgcgcct gagatgaaac 600  
 aggggtgcggg tgcacgtgg agtcattcca agactctgt cctcactcag 650  
 ggattcttca tttctctctc ctactgcctc cacttcattgt tattttcttc 700  
 ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750  
 tottggtctc ctcttactc ccattctggac ccagtcctct ggttctctgc 800  
 tgtttattgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 340  
 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala  
 1 5 10 15  
 Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val  
 20 25 30  
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
 35 40 45  
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
 50 55 60  
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
 65 70 75  
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
 80 85 90  
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
 95 100 105  
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
 110 115 120  
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
 125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtraggcgc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatactgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtgpatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg cccataatca ggccagccctc atcagtcgct gtagc 45

(210) 346

(211) 2575

(212) DNA

(213) Homo sapiens

(400) 346

tcttacctga ctggaagcgt ccaaaagagg agggctgtca gacctgcttg 50

actjagaacc caccagctca tccagacac ctcatagcaa cctatcttata 100

caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa cgggggtaaa gggagggag caattcaatt tgaagtccct 200

gtgaatgggc ttccagaagg caattaaaga aatccactca gagaggactt 250

ggggtgaaac ttgggtccctg tggttttctg attgtaagtg gaagcaggtc 300

ttgcacacgc tgttggtcaa tgtcaggacc aggttaagtg actggcagaa 350

aaacttcacg gtggaacaag caaccatgt tctgtgcaa gottgaagga 400

gacctggagc ggagaaagct aacttgaaca tgacctgttg catttggcaa 450

gttcctagcaa catgtctcta aggaagcgat acaggcacag accatgcaga 500

ctccagttcc tctgtctgt cctgatgctg ggatgcgtcc tgatgatggt 550

ggcgatgttg caccctcccc accacacct gcaccagact gtcacagccc 600

aagccagcaa gcacagccct gaagccaggt accgcttga ctttggggaa 650

cccaggatt ggttactgga agctgaggat gagggtgaag agtacagccc 700

tctggagggc ctgcacacct ttatctcact gggggaggat cagctgctgg 750

tggcctggtg cttaccccag gccagaagga accagagcaa gggcaggaga 800

ggtgggagct accgctcat caagcagcaa aggaggcagg ataaggaagc 850

ccaaaagagg gactggggg ctgatgagga cggggagggt tctgaagaag 900

aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950

agtgcocgca tccccctcca gagggctctg cccgaggtgc ggcaccactc 1000

gtgtctgcag cagcaccctc aggcagcct gccacagcc agcgtcatcc 1050

tctgtttcca tgatgaggcc tggtcacctc tctgcggac tgtacacagc 1100

atctctgaca cagtgcocag ggccttctct aaggagatca tctcgtgga 1150

cagctcagc cagcaaggac aactcaagtc tctctcagc gaatatgtgg 1200

ccaggctgga ggggtgaag ttactcagga gcaacaggt gctgggtgac 1250

atcagggccc ggatgctggg ggcaccaga gccacgggg atgtgcttgt 1300  
 cttcatggat gcccaactgg agtgacaccc aggtgagctg gagccctccc 1350  
 ccagcagaat agctggtgac aggagccgag tggatatccc ggtgatagat 1400  
 gtgattgact ggaagacttt ccaglattac cctccaaagg aactgcagcg 1450  
 tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500  
 atgtgaggaa ggccctccag tccccataa gccccatcag gagccctgtg 1550  
 gtgcccggag aggtgggtgc catggacaga cattaactcc aaaacactgg 1600  
 agcgtatgac tctcttatgt cgcctgcgagg tggtgaaaac ctcgaaactgt 1650  
 ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700  
 cgggtaggac acatctacca aaatcaggat tccattccc cctcgacca 1750  
 ggaggccacc ctgaggaaac gggttcgcac tgcagagacc tggctgggg 1800  
 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctcttgagc 1850  
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
 ggggtgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
 acccatctga acccaggccc agtttctctg gaaagctcca caaacctgga 2000  
 cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050  
 catggtgttg gctccttgca gtgacagccg gcagcaacag tacttgagc 2100  
 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150  
 gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200  
 ggcacccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250  
 acattctttc tgggaaatgc atggaagctg tgggtgcaaga aaacaataaa 2300  
 gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350  
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400  
 aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450  
 atatatttca tgaagctgat ctttttgtgt gtgtgctcct tgtgttagga 2500  
 gagaaaaaag ctctatgaaa gaatatagga agtttctcct ttccacacct 2550  
 tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
1				5					10					15	
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val  
 560 565 570

Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln  
 575 580 585

His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser  
 590 595 600

Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu  
 605 610 615

Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe  
 620 625 630

Asp Gln Ile Asn Ala Val Asp Glu Arg  
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<210> 348

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcaactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtcgtg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2524

<212> DNA

<213> Homo sapiens

\*410\* 351

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tccctctctg gccactgatg ttgatgcacc tcccacccgc tgcacagggc 150  
tcttcactct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtg 200  
caggggagga cctcgggccc caggtcattg gtgagtgtag gagcgagcac 250  
ctccaccaag ccgatctcct egggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcaactg cccccccagc ccccccatca ggctttgagg aggggcgcgc 350  
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tttgacagccc ctcatgggct cgcaacccca cccccaaat cagaactccat 500  
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gacagctgtg gtagagctgg gccacagggg ctctggctc ctgcctctt 1400

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 cctggctgtc tgtgtgtgtg ccattctctg gacttcagag ccccctgagc 2150  
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20			25						30	

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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cgtgcccacg ctgtggaaag agccggccga gctgcccctg ggagaaggcc 200  
 ccgtggagag caccagcccc ggcggggagg ccgtggacac cggcccccca 250  
 gccccacccg tcgcgccagg acccgaggac agcaccggcg aggagcggct 300  
 ggaccagggc ggcggtgcgc tggggcccggt cgtatcgccg gccatcgtga 350  
 tcgcgcacct gctggccacc tgcgtggtgc tggcgtcgtt ggtcgtcgcg 400  
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 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PFT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120  
 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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 gttggccggc ggcgggccgg gacgggcctg gccctgtatc tgtgctggt 100

gtgootgaag gggggggtgg cccacgggtg totgpaatgc cacagcaact 150  
tctccaagaa gttctctctc taccggcacc atgtgaaact caagtcootgg 200  
tgggtggggg acatccccgt gtcagggggg ctgctcaccg actggagoga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat tccccaaag agctgogaaa 400  
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggagggg agctctccag ggagggacc 500  
agcctagcac ctgaaggatc aatgpcatca ccccggggg acctcccta 550  
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tgctccatct cactctgggg gtcaacctgg ggaaccttc cctccggggc 650  
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tggcatcttc cagtaagaga ccatctcttg caacaactgc acagactcgc 750  
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accogtgcca gggccctact gtccctgggg tcccaggctc tcttggagg 850  
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cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100  
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 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg ccccagggga acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg acccctctc 2000  
 cgacccccga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcttgggcag gtccgcagag 2100  
 ctgogggatg tgattaaagt cctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

125

130

135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro  
 140 145 150

Ser Pro Arg Gly Asp Leu Pro  
 155

&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

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 ttgagaaatc ctccagatggc cctgggtgctg cccaggaacc cactgggttc 150  
 acagatgtcc cagctggccat ggaattcatt gctgcactg aggtggctgt 200  
 cataggcttc ttccaggatt tagaaatacc agcagtgccc ataactcata 250  
 gcatgggtgca aaaattccca ggogtgtcat ttgggatcag cactgattct 300  
 gaggtttctga cacactacaa catcactggg aacaccatct gctctttctg 350  
 cctggttagac aatgaacaa tgaatttaga ggacgaagac attgaaagca 400  
 ttgatgccac caaattgagc cgttttcattg agatcaacag cctccacatg 450  
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 tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550  
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 catgtgcaaa acttttctga tggattccta agtggaaaat tgttgaaaga 800  
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaaact tgaattctcc 850  
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 aactcaaatc tcagagacac taaacaacag gatcactagg cctgcacaac 950  
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 tctctctctt ctctctttta atttcatac ctcaactcct atcaatttc 1100

atttattatcg tgcattcata ctctgtaagc ccattctgtaa cacacctaga 1150  
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 cttagagaaag attgttcbaa tttgtcattt aatatcaagt ttgtatactg 1250  
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 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaacca aaggatggtt ttaaaccact ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggtctgtct caagtccctg aactcagcag aaatagacca 1450  
 tgtgaaaact ccattgcttg tttagctctc caactcccta tgtaaataca 1500  
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
			20					25					30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
			35					40					45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
			50					55					60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
			65					70					75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
			80					85					90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
			95					100					105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
			110					115					120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
			125					130					135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
			140					145					150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
			155					160					165	

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180

Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210

Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225

Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240

Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255

Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

ccagcagtgcc ccatatccca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tjagagtggtg gatacaatgc 20

<210> 361

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gattatagga aatttttgtgt gtgg 24

<210> 362  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 362  
tattccaggc gtgtcatttg ggatcagcac tgattatga; gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
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ccggcgccggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100  
cctcagccggg gacccgggct cagggacgcg gcggcgccgg cggcgactgc 150  
agtggctgga ccatggcagc gtccgcggga gccggggcgg tgattgcagc 200  
cccagacagc ccggctcggc tctggctcgt gctggcgccg gcgcttgggc 250  
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tagtaagact ggcgggctga cctcagcttc ctggagcttc cagccagagg 400  
gggcgcacac taatgtgtcg tttttccact acctcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcacaa tcaacataga aaatatgcag tttatacaca 550  
atggcaccta tatctgtgat gtcaaaaaac ctctgacat cgttgtccag 600  
cctggacaca ttaggtctca tctcgtagaa aaagagaatt tgcctgtgtt 650  
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ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaaagggatt acaatggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct ccgaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900  
tccggcgagc atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgccgatata ccgaagaatt aaagaaata ctagaatata tctccagcaa 1000

gaaacaaaaa caaactggac tctcgtgcag aaaatgtagc caattaccac 1050  
 atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatattga taaatattct atttagtcac 1150  
 cctgatatga ggagccagtg ttgcattgat aaaagatggt atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattc agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400  
 tggaggatgg agatgctatg atggaagcat acccaggggt gccttttagca 1450  
 cagtatcagt accattttatt tgtctgcgcg ttttaaaaaa taccattgg 1500  
 ctatgcacac tgaaaacaat ttgagaagtt tttttgaagt tttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcacccg tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggttttta 1777

<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
 1 5 10 15  
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
 20 25 30  
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
 35 40 45  
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
 50 55 60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
 65 70 75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
 80 85 90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	
				95					100					105	
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	
				110					115					120	
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	
				125					130					135	
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	
				140					145					150	
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	
				155					160					165	
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	
				170					175					180	
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	
				185					190					195	
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	
				200					205					210	
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	
				215					220					225	
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	
				230					235					240	
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	
				245					250					255	
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		
				260					265						

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gcaggctgtg cagagaagcc atgtaccggc tctgttcagc agtgactgcc 5'  
 cgggctgcgc ccccccggggg cttggcctca agctggggac gacgcggggg 100  
 ccataagcgc gccgggctgc cgcctctcgg ccacggctgg gtccgggggc 150  
 tcgggctggg gctggggctg ggcctcgggg tgaagctggc aggtgggctg 200  
 agggggcggg cccggggcga gtcccccgcg gcccccagacc ctgaggcgtc 250  
 gcctctgggc gagccgcac agggagcagtc cctggccccg tggctctcgc 300  
 agacccccgc gccgcctgc tccaggtgat tcggcagagc cctcgagagc 350  
 agccgggacc tgtgcacag gatcaaggat gagggtgggg caccggggcat 400

agtgggttggga gtttctgttag atggaaaaga agtctgggtca gaagggtttag 450  
 gttatgctga tgttgagaa cgtgtaccat gtaaacacaga gacagttatg 500  
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgcacaaatt 550  
 gtgggaagca gggaaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgcacaaca 650  
 agattactga ttcccatctt aagtgggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgcgggaa 850  
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat cctaagatt atttaaaaaat 950  
 gatcttttgt tcttcaaac ttgttagtcag tttttgtatt caacttttgg 1000  
 ctataacctc ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgaat tggatatgt gacgaactgt 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150  
 ctctctgtgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcacaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

\*210\* 366  
 \*211\* 373  
 \*212\* PRT  
 \*213\* Homo sapiens

\*400\* 366  
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
 1 5 10 15  
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
 20 25 30  
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
 35 40 45  
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
 50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
365 370

<210> 367  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<210>  
<213> Synthetic oligonucleotide probe

<400> 367  
tggaagagaa gtctggtcag aaggtttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<210>  
<213> Synthetic oligonucleotide probe

<400> 368  
catttggtt cattctctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<210>  
<213> Synthetic oligonucleotide probe

<400> 369  
aaaacctcag aacaactcat ttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<210>  
<213> Synthetic oligonucleotide probe

<400> 370  
ttctaccat ggttgettt gccaaattgt gggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
ttgacactat agaagagta tgaagtgca tgaagtgta cgttaagctg 50



Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	
				35					40					45	
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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ggtgggccc ctatggccc agtgtccc ggtgtccc gagacgggg 100

cagcaggctcg tccggggggcc caccatgctg gtgactgctt acccttgctt 150  
tgttaggcctc ctggcctcct gcttggggct ggaactgtca agatgcgggg 200  
ctaaaccccc tggaagggcc tgcagcaatc cctccttctt tcgggttcaa 250  
ctggacttct atcaggctca ctctctggcc ctggcagctg attggcttca 300  
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
aaattgccat cctctatgtc tgttgccttg cctctacagt cctctttggc 400  
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
cctcttctcc ctgaacttact cactatgctg cttaaccaaa ctctctcaag 500  
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
ctgctcttct cagccttcga ggctgggtat atccatgagc acgtggaacg 600  
gcctgacttc cctgctgagt ggatcccagc tacctttgct cgagctgctt 650  
cttggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
gcagctgga tagggctggg gcctgtagcg ccttttgttg ctgcctccc 750  
tctctggct ctggcagggg ccttggcctt tcgaaactgg ggggagaact 800  
atgacggga gctgctcttc tcaaggacct gtgctggagg cctgcctgct 850  
ctctgtcgg accgcgcgct gctgctgctg ggcaccatac aa jctctatt 900  
tgagagtgtc atcttctctt ttgtcttctt ctggacacct gtgctggacc 950  
cacagggggc cctctgggc attatcttct ccagcttcat ggcagccagc 1000  
ctgcttggct ctctcctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
tcagcccatg caactgctgt ccttgcctgt gctcctgctc gtcttctctc 1100  
tcttcatgtt gaatttctct accagcccag gccaggagag tccggtggag 1150  
tcttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200  
cagcatgagc ttctacgga gaaaggctgat cctgagaca ggcaggctg 1250  
gtgtactcaa ctggttccgg gtaacctgct actcactggc ttgcctaggg 1300  
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
cagcatttgc tctgctgtca tgggtgatggc tctgctggca gtgggtggac 1400  
tcttcccgct ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
gaggagcct atgcctctga gctgtaacct cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgaacttt gtgaactgtcc tgtgggtttct cctggcattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650  
 ctctgtgtta ctcccattta gaaaataaac accttttaaat gatcaaaaaa 1700  
 aaaaaa 1706

<210> 374  
 <211> 450  
 <212> PRT  
 <213> Homo sapiens

<400> 374  
 Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser  
 1 5 10 15  
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
 20 25 30  
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
 35 40 45  
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
 50 55 60  
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
 65 70 75  
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
 80 85 90  
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
 95 100 105  
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
 110 115 120  
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
 125 130 135  
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
 140 145 150  
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
 155 160 165  
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
 170 175 180  
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
 185 190 195  
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
 200 205 210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

tcgacgcgcg gggggggggc gagaggaaac ggggggcggg gccgggcccg 50

ggcctggaga tgggtcccggt cggcgggggg tgggtgttgtc tgggtgatctg 100  
 ggtcccggtg tgggtcggtg cccaggggtt cgggtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatcacatctt cccagccaca 200  
 cctggccaagg actttgggtg tatctttcac acaagggtatg agcagattca 250  
 ccttgtcccc gctgaacctc cagaggcctg cgggggaactc agcaacgggt 300  
 tcttcaccca ggaccagatt gctctgggtg agaggggggg ctgtccttc 350  
 ctctccaaga ctgggtggt cccaggagcac ggcgggcggtg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaacca ggcacagct gacatccccg cctcttctct gctcggccga 500  
 gacggctaca tgatccggcg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atccagtc aatgtccag catccccacc tttgagctgc 600  
 tgcaacggcg ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgaat ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
 tttgggggtt gctaggctga aagggaagcc acaccactgg ccttccttc 800  
 cccagggccc ccaaggggtg ctcatgctac aagaagaggg aagagacagg 850  
 ccccaggggt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900  
 gcttgagage catctgtgac ctgtcacact cactgggtc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagtttgt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050  
 taagcttct catcaggggt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

\*210\* 376

\*211\* 188

\*212\* PRT

\*213\* Homo sapiens

\*400\* 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25					30	

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40					45	

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	
				50					55					60	
Gln	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	
				65					70					75	
Gln	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	
				80					85					90	
Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln		
				95				100					105		
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp	
				110					115					120	
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg	
				125					130					135	
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr	
				140					145					150	
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile	
				155					160					165	
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu	
				170					175					180	
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp								
				185											

\*0210\* 377  
 \*0211\* 496  
 \*0212\* DNA  
 \*0213\* Homo sapiens

\*0220\*  
 \*0221\* unsure  
 \*0222\* 396  
 \*0223\* unknown base

\*0400\* 377  
 actgactcca ctgctctgtg ctgggacat ggaacttgca ctgctgtgtg 50  
 gggtgggtgt gatggctggg gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccttac ggctgtcact ggggactagg tggcagaggg caaccacaag 200  
 atgcaacgga ctgggtgtgc cagacccatg actgctgcta tgaccactg 250  
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 496

<210> 378  
<211> 116  
<212> PRT  
<213> Homo sapiens

<400> 378  
Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val  
1 5 10 15  
Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys  
20 25 30  
Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly  
35 40 45  
Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr  
50 55 60  
Asp Trp Cys Cys Glu Thr His Asp Cys Cys Tyr Asp His Leu Lys  
65 70 75  
Thr Glu Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile  
80 85 90  
His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe  
95 100 105  
Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu  
110 115

<210> 379  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 379  
ctgactccac tgcctctgtgc tggg 24

<210> 380  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 380  
cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45  
<212> DNA  
<213> Artificial Sequence

<221>  
<223> Synthetic oligonucleotide probe

<400> 381  
ctgaacaaga tggtaagca agtgaatggg aaaatgccc tcttc 45

<210> 382  
<211> 764  
<212> DNA  
<213> Homo sapiens

<400> 382  
ctcgtttctt cttcttggat gggggcccag gggggccagg agagtataaa 50  
ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100  
gcccgtgggat gcacgggcca gaggccatgc tgctgctgct cactgttggc 150  
ctctgtgggg gcccacactg ggcagggaag atgtatggcc ctggaggagg 200  
caantatttc agcacactg aagactacga ccattgaaatc acagggtctgc 250  
gggtgtctgt aggtcttctc ctgggtgaaaa gtgtccaggt gaaacttgga 300  
gaactctggg acgtgaaact gggagcctta ggtgggaata ccagggaagt 350  
caccttgcag ccaggcgaat acatcacaaa agtctttgtc gcttccaag 400  
cttctctcgg gggataggtc atgtacacca gcaaggacgg ctatttctat 450  
tttgggaagg ttgatggcca gatctctctt gctacccc gccaagaggg 500  
gcaagtgtgt gtgggcact atggccagta tcaactcctt ggcattcaaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaate tccatactc agcaaaactc ccgtgggtc gctaggggtg 650  
ggtatggggc catccagct gaggccatct gtgtgggtgt ggctgatggt 700  
acttgagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383  
<211> 178  
<212> PRT  
<213> Homo sapiens

<400> 383  
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	20	25	30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	35	40	45
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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agctctgtgg ctgaactggg tgctcatcac gggaactgct gggtatgga 100

atacagatgt ggcagctcag gtagccccc aaattgctgga agaatacatc 150

atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaacgcg 200

ccctccccc ccccccaaaa aaactgtaaa gatgcacaaa cgtaatatcc 250

atgaagatcc tattaactag gaagattttg atgttttgcg gogaatggcg 300

tggtgggatt tatttgttct tggagtgttc tgcgtggctg gaaaagaata 350

atgttccaaa atcgggtccat ctcccaaggg gtcccaatttt tottctggg 400

ctcagcgag ccctgactca ctacagtcca gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc ttggaacaat 500  
acaaaggatg ggtttcaatg taattaggt aotgagggga tcagctgtag 550  
caatgggtat agcccccact gtcttactga caatgctttt ttctgcccga 600  
cgaggatgac ctaagggctg taggtgtgaa ggcaaaatg tatattgtga 650  
atctcagaaa ttacaggaga taccctcaag tatatctgt ggttgcttag 700  
gtttgtccct tegtataac agcttccaa aacttaagt taatcaattt 750  
aaagggtcca accagctcac ctggtatata cttgaccata accatatcag 800  
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
ttcttagttc caatagaatc tctattttt ttaacaatac cttcagacct 900  
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
gggatctgaa cagtttcggg gcttgccgaa gctgctgagt ttacatttac 1000  
ggctataact cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100  
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagaccat 1250  
gtcttgacc tggagctcct tacaaggct tgatttatca ggcaatgaga 1300  
tcgaagcttt cagtggacc agtggttttc agtgtgtccc gaatctgcag 1350  
cgctccaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400  
ggattcttgg atatccctca atgacatcag tottgctggg aatatatggg 1450  
aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500  
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650  
cccaagctcc ccaggccgaa gcattgagag aaacccccct tgcctccgac 1700  
ggtgggagcc acagagcccg gccagagac cgatgctgac gccagacaca 1750  
ctcttttcca taaaatcacc gggggcagcg tggcgctttt cctgtccgtg 1800  
ctcgtcacc tctgtgttat ctaagtgtca tggaaagggt accctgcag 1850  
tatgaagcag ctgagcaga gctcctcat gggaagatc atgaaaaa 1900

aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950  
 gattataaac ccaccaaac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtcttta 2100  
 tgaactctg gtgactatca agggaaacgg atgccccccc tccccctccc 2150  
 tctccctctc actttgggtg caagatcctt ccttgctcgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccttttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385  
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala  
 1 5 10 15  
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala  
 20 25 30  
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150

Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	
				155					160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	
				170					175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	
				185					190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu	
				200					205					210	
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	
				215					220					225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	
				230					235					240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	
				245					250					255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	
				260					265					270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	
				275					280					285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	
				290					295					300	
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	
				305					310					315	
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	
				320					325					330	
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	
				335					340					345	
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	
				350					355					360	
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	
				365					370					375	
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	
				380					385					390	
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	
				395					400					405	
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	
				410					415					420	
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	
				425					430					435	

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
 440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
 455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
 470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
 500 505 510

Cys Glu Val

\*210\* 386

\*211\* 24

\*212\* DNA

\*213\* Artificial Sequence

\*220\*

\*221\* Synthetic oligonucleotide probe

\*400\* 386

ctcgcgatctg aacagtttcg gggc 24

\*210\* 387

\*211\* 24

\*212\* DNA

\*213\* Artificial Sequence

\*220\*

\*221\* Synthetic oligonucleotide probe

\*400\* 387

ggctccctagg acatggtctg tccc 24

\*210\* 388

\*211\* 48

\*212\* DNA

\*213\* Artificial Sequence

\*220\*

\*221\* Synthetic oligonucleotide probe

\*400\* 388

gctcagtttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

\*210\* 389

\*211\* 1449

\*212\* DNA

\*213\* Homo sapiens

\*400\* 389

gtttctgaga aagaaggaaa taaacacagg caccaaaacca ctatcctaag 50  
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtoacctca 100  
ggatcttcaa ccatagggat ctgtgttttg ccgtattcc agttgggtgt 150  
ctcggaccta ccatcggaag aagatgaaat gtgtgtaaat tataatgacc 200  
aacaccttaa tggctggtat atctggatcc tctgtgtgt ggtttttggtg 250  
gaagctcttc tctgtggagg tgtggtcttc tgcctcagtt gctgggtgag 300  
gagacccoga attgattctc acaggcgcac catggcagtt tttgtgttg 350  
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400  
ggaattcacc ttcaaaactca aaccttgac ctatctctg ttctgtctcc 450  
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500  
caacctgatt ttaggtgttg attatcaatt taaagtatta acgacatctg 550  
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700  
aggcttttga tgtgtcactg ctgtatcata cttttatgt acacaaccaa 750  
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
gtagtttcca ccacatttag gactccactg cagtatacag cacaccattt 850  
tctgctttaa actctttcct agcatgggtt ccataaaaaat tattataatt 900  
taacaatagc ccaagccgag aatccaaat gtccagaacc agaaccagaa 950  
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
tgagagtgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100  
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttccct tttacagtaa tgaatgtggc 1200  
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250  
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
ctgacaaatt ttttaaaaaa aacaataaac atcaatgat atctaaaaa 1449

<210> 390  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr  
           1                  5                  10                  15  
 Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp  
                   20                  25                  30  
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
                   35                  40                  45  
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu  
                   50                  55                  60  
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
                   65                  70                  75  
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
                   80                  85                  90  
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
                   95                  100                  105  
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
                   110                  115                  120  
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
                   125                  130                  135  
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
                   140                  145

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 attttcagtg tcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392

ccaaaaatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccatttggtg ctctgggacc taccatgga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50

acccacccgc gttctctccag ctgatcttg aggctgttc gccagtgtgg 100

gacgcagctg acgcccgcgt attagctctc gctgcgtcgc cccggctcag 150

aagctccgtg ggggggggga ccgtgacgag aagcccacgg ccagctcagt 200

tctctctcac ttggggagag agagaaagtc agatgcccc tttaaactcc 250

ctcttcaaaa ctcatctctt gggtagctga gttaatagag tggatacaac 300

cttctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350

ttttcaagtc ttgatttggt gcttacctca agttaccatt ttccagtcac 400

gtctgtttgt ttgcttcttc agaaatgttt ttacaactc caagaaaaaa 450

tatgtcccag aaattgagtt tactgttgc tgtatttgga ctcatgtgg 500

gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550

gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600

tctagcagag gaaaataaga acacagtggg tctcgagaac ggtgcttcta 650

tggcaggata tgcggatctg aaaagaacaa ttgtgtctct ctgggatgac 700

atttttgaac gattggtgaa gctggagaa aaagttgact atattgttgt 750

gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800

cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850

ttgaaaatca ccttgtgctg ctccatccac tgtggattat atctatggc 900

agaaaagctt tataattgct ggttaggac agagcaatac ttacaataa 950

aagctctaca cactttcaag gactatgctg gattcatgga actctaatc 1000  
tgtacataaa aattttaaag ttatttggtt gctttcagga aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100  
aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
aaatgaaaaa actgaaaaa atggattcat ttctataaca catttattta 1200  
agtatataac acgttttttg gacaagtcaa gaatgtttaa tcattctgtc 1250  
atttgttctc aatagatgta actggttagac taaggctatt tgaaaaaatg 1300  
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tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400  
tttgcactat ccttcagaat aactgaaggc taattattgt atatttttaa 1450  
aaattacact tataagagta taatcttgaa atgggttagca gccactgtcc 1500  
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550  
gtaaaactca atcttatact tattgaagaa taaaagatat ttttatgatg 1600  
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650  
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700  
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tttgaggaat ggaactcttg aggactttag ccagggtgtat ataataaagg 1800  
tacttttgtg ctgcattaaa ttgcttgcaa agtggttaaca ttatattata 1850  
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950  
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
atttcccttg tagcaaatct aattgccaca tgggtgccta tatttcatag 2100  
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150  
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300  
acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10						15
Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20				25						30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35				40						45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50				55						60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65				70						75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80				85						90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95				100						105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110				115						120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
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Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396

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<210> 397  
 <211> 353  
 <212> PRT  
 <213> Homo sapiens

<400> 397  
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 35 40 45  
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
 50 55 60  
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
 65 70 75  
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
 80 85 90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe Ser
95	100	105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly Leu
110	115	120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser Asp
125	130	135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser Ala
140	145	150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu	
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<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgcccagc ccagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggtaggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caacccccag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatgggcag ccacagcttc tgtgagatc gattttctcc cagttccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaaggg 100

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atgcattct ctatctatc actgcaagt cctgctgttc caggccttac 200

ctgtgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

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 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 agtgggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccaccccag tagactccc agtcccataa ttgtgtatct tccagcccag 1500  
 aatccacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

(210) 402

(211) 261

(212) PRT

(213) Homo sapiens

(400) 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25					30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40					45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
				95					100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
				245					250					255
Trp	Met	Glu	Glu	Thr	Glu									
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<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctctgtgtgt ctccagattt cagggcta 29

<210> 404  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
agtcctcctt aagattctta tptcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
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gtccgggtgc ggggcctacg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tgcactccaa atgcaaggag aagcagctct tgcctgggtg 200  
ggagacgggtg caagagaatc tgccccctat aggggaatgg tggccacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
cacccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350  
tatgaacatc cccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
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gctgggtacc caatatacaa agagcagcac tgggtgaatat gggagattta 650  
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ggacaatata atgactcacg gtttatcaag tttatgttct ggactggtag 750  
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ctgcttgatt caggctgttc aagggtgaagg attcatgagt ctatataaag 900  
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<210> 406  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln	1	5	10	15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	20	25	30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	35	40	45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	50	55	60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	65	70	75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	80	85	90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	95	100	105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	110	115	120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	125	130	135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	140	145	150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	155	160	165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	170	175	180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	185	190	195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	200	205	210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	215	220	225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	230	235	240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	245	250	255	

Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr
				260					265					270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly
				275					280					285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met
				290					295					300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg
				305					310					315
Glu	Met	Ser	Gly	Val	Ser	Pro	Phe							
				320										

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgaggatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ggggaattct taaaatggac tgactccact cacc 34

<210> 409

<211> 1437

<212> DNA

<213> Homo sapiens

<400> 409

gggacgggtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcttgcggcg gcgcctgaag tcggcggtgg cgtttgagga agctgggata 100

cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150

tagataatct tcgttgccca gaatgtgaat gtattgactg gactgagaga 200

agaaatgctg tggcatctgt tgtgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tccaaagcca gaacagttga 300

accatgcttt ccacacatgt ggtgtatttt ccacattggc ttctctcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
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 cataaaagggt tttcagcaag ttgttaacta ttttggcta aaaatgaggt 1350  
 ttttttgta aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20				25					30	

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
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<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 411  
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<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccagaaactoga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<410> 413

atgggcaggct tctagataa tttctgttgg ccagaatgtg 40

<211> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<410> 414

gttgatggca aatttcttca aaggaggggc agagctgtgg cagggcagga 50

gcagctggcc cactgggggc ccgcaacct ccgtctcacc ctctggggcc 100

actgcattca gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtgggtggc agctgggtca 200

gggacctacg gcacctgtgt gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccaccttc 300

acctggacag gatgagagtg tcaggtgtgc ttcgctctct ggccctcacc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaaac atccgtctgc cactgtggct ggcagccctg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcattcaagg ctgcccagcc 500

aactactttg cgttttaaat ctgcagtggg gcgcaccaag tctgtgggccc 550

tactatgtgc tttgaagacc gcattgatcat gactctgtgt aaaaaaatg 600

tgggcagagg cctaaacatc gccctgggtg atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaatto cgggggggtgc actggtgtgt gtggcctctt 750

acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800

gaattgggga gttcttaccg aaaaacaactg ggcttcgggg acagctgggt 850

cttcattagga gccaaaagac tcaggggtaa aagcccttt gagcagttct 900

taaagaacag ccagacaca aacaaatacg agggatggcc agagctgtgt 950

gagatggagg gctgcattgc ccgaagcca ttttaggggt gctgtgggtc 1000

ttctcagcc aggggcctga agaagctctt gctgactta ggagtcagag 1050

ccggccaggg gctgaggagg aggagcaggg ggtgctgcgt ggaagggtgt 1100

gcaggctctt gcacgtgtgt tcgcgctctt cctctctgga aacagaaccc 1150

tccacacaa cactctaccc ggaagaccag cctcagggg tctttctgga 1200

accagctgtc tctggagaga atggggtgct ttcttcaggg actgctgacg 1250

gtcggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300

tatttttgcg ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala
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Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser
				20					25					30

Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr
				35					40					45

Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro
				50					55					60

Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala
				65					70					75

Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met
				80					85					90

Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu
				95					100					105

Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp
				110					115					120

Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu
				125					130					135

Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro
				140					145					150

Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu
				155					160					165

Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val
				170					175					180

Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln
				185					190					195

Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro
				200					205					210

Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	
				215					220					

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 416  
ggcattatcca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 418  
aaagtacaag tgtggcctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 419  
tatgattcct aagtcaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421

<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
gtacaagtgt ggcttcacca agccctgccc agccaactac ttggcg 46

<210> 421  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1529  
<223> unknown base

<400> 422  
gagaactgcag agggagataa agagagagggg caaagaggca gcaagagatt 50  
tgttcctgggg atccagaaaac ccattgatacc ctactgaaca ccgaatcccc 100  
tggaaagccc aagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgcacgga gctcgtctgc totctctctc totctctcac tctcctctcc 200  
ctctctctct gcttgctcta gtcctctagt cctcaaatc ccagtccct 250  
gcaccccttc ctgggacact atgttgctct ccgcctctct gctggagggtg 300  
atttggtacc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggctcag gacatttggc cagcctctta cctgagtggt ggaaacaatg 400  
cccagtctcc catgatatt cagacagaca gtgtgacatt tgacctgat 450  
ttgctgtctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtcca actctctctg cctctaccc 550  
tgtatctggg tggacttccc cgaatatatg tagctgccc gctccacctg 600  
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
tgaagccaca ttgcagagc tccacattgt acattatgac ttgattcct 700  
atgacagctt gactgaggct gctgagaggc ctccaggcct ggctgtcttg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
ctgagtcac ttgatgaag tcaggcataa agatcagaag acctcagtgc 850  
ctcccttcaa cctaagagag ctgctcccca aacagctgg gtagtacttc 900

ggtacaaatg gctcgctcac aactccccct tgcataccaga gtgtgctctg 950  
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaaga 1000  
 ttcaggggac attgtttctc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gctctcaat cagcgcctgg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
 gtgtaggaat cttgggttggc tgtctctgcc ttctctggc tgtttatttc 1200  
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 cttcacctca gcacaagcca cgactgaggg ataaattcct tctcagatac 1300  
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 ggggtgtaga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
 ccttccccctg gacatctctt agagaggaat ggaccagggc tgtcattcca 1450  
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
 gaaatcgtg tgttggtaat gcagagacca aactctgttt agttgcaggg 1550  
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
 tttccctaga tatactgggg gatctctcct taggataaag agttgctgtt 1650  
 gaagttgtat attttggatc aatatatttg gaaattaaag tttctgactt 1700  
 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 423  
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
 1 5 10 15  
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
 20 25 30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Glu  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala
95	100 105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly	
110	115 120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His	
125	130 135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala	
140	145 150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu	
155	160 165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His	
170	175 180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro	
185	190 195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe	
200	205 210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val	
215	220 225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln	
230	235 240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro	
245	250 255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn	
260	265 270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr	
275	280 285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly	
290	295 300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile	
305	310 315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser	
320	325 330
Ala Gln Ala Thr Thr Glu Ala	
335	

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 424  
gtaaagtgcg tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 425  
cccgatctgc ctgctgta 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 426  
ctgcactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 427  
cagaaaacca tgatacccta ctgaacacccg aatccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
aatttttcac cagagtaaac ttgagaaaac aactggacct tgagtattgt 50  
acattttgcc tegtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150  
aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200  
ctaccaaacc aacagcagtc aaatcaggto tttccttctt taagtctgat 250  
accattaaca cagatgctca cactgggggc agatctgcat ctgttaaata 300

atgctgcagg aatgacacct ggtaccaga cccaccatt gacctggga 350  
 gggttgaatg tacaacagca atgacacca catgtgttac caatttttgt 400  
 acacaaactt ggagccbagg gaactatctt aagctcagag gaattggcac 450  
 aaatottcac gagctccttc atccattctt tgttccggg aggcattctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcaggtgtta atcttgcac ccagggaacc ccagcaggcc 600  
 gctcccaaac tcccagtggc acagatgacg actttgcagt gaccacctct 650  
 gcaggaatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaattgga attcagtaag ctgtttcaaa ttttttcaac taagctgctt 750  
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatatct ttgaaatttc agaaaatatg ttctatgtag agaattccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgctgctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75  
 Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn  
 80 85 90  
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

95	100	105
Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
110	115	120
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly		
125	130	135
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp		
140	145	150
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln		
155	160	165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
170	175	180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
185	190	195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
200	205	

(210) 430  
 (211) 1257  
 (212) DNA  
 (213) Homo Sapien

(400) 430  
 ggagagagaggg ggggggggtga aaggggcatt gatgcagcct gggggggcct 50  
 cggaggggggg cggagggcaga cggcgaccac gttcctctcc tcgggtctcct 100  
 ccgcctccag ctccgggctg ccgggcagcc gggagccatg cgaacccagg 150  
 gcccggcggc ctcccggcag cggctccggg gctcctgtct gctcctgtctg 200  
 ctgcagctgc ccggggcgtc gagggcctct gagatcccca aggggaagca 250  
 aaaggggcag ctccgggcaga gggaggtggt ggacctgtat aatgggaatgt 300  
 gattacaagg gccagcagga gtgcctggtc gagaaggagg cctgggggpc 350  
 aatgtttatto cgggtacacc tgggatccca ggtcgggatg gattcaaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgggg agtgtacatt tacaaagatg cgttcaaata gtgtctaaag 550  
 agttttgttc agtggctcac ttgggtataa atgcagaaat gcatgtctgc 600  
 agcgttggtt ttacacattc aatggagctg aatgttcagg acctcttccc 650  
 attgaagcta taatttattt ggaaccaagga agcctgaaa tgaattcaac 700

aattaatatt catggcaatt ctctctgtgga aggaatttgt gaaggaaattg 750  
 gtgctggatt agtgggatgtt gctatctggg ttggcaattg ttcagattac 800  
 ccaaaaaggag atgottctac tggatggaat tcagtttctc gcatcattat 850  
 tgaagaacta ccaaaaataaa tgccttaatt ttcatttgtt acctcttttt 900  
 ttattatgco ttggaatggg tcaactaaat gacattttaa ataagtttat 950  
 gtatacatct gaatgaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
 tgatttcaca ctgttttttaa atctagcatt attcattttg ctccaatcaa 1050  
 aagtggtttc aatatttttt ttagttgggtt agaatacttt ctccatagtc 1100  
 acattctctc aacctataat ttggaatatt gttgtgggtct ttgttttttt 1150  
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
 aatttgtaaa tgttaagaat tttttttata tctgttaaatt aaaaattatt 1250  
 tccaaca 1257

<210> 431  
 <211> 243  
 <212> PRT  
 <213> Homo Sapien

<400> 431  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15  
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aggaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgaggctcg tacaaggcaa c 21

<210> 435  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 435  
gggaccgta ccaccatgt 19

<210> 436  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 436  
actccaggca ccattgttgc tccc 24

<210> 437  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 437  
aagggtctggc attcaagtc 19

<210> 438  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 438  
tgacctggca aaggaagaa 19

<210> 439  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 439  
cagccacct ccagtccaag g 21

<210> 440  
<211> 19

<210> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gaggaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tctcccatca cttcccttag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

agortacaat ctctccagga aaccag 26

<210> 446

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 446

caattctgga tgaggtgga ga 22

<210> 447

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 447

caggactgag cgcttggtta 20

<210> 448

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

caagagcgcca agtacggac c 21

<210> 449

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

ccagactca gccaggaa 18

<210> 450

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccctagctga ccccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctgacaagc agttttctga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccccc ccccttttct ttgttt 26

<210> 453

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctgttgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

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